

(1 of 90)

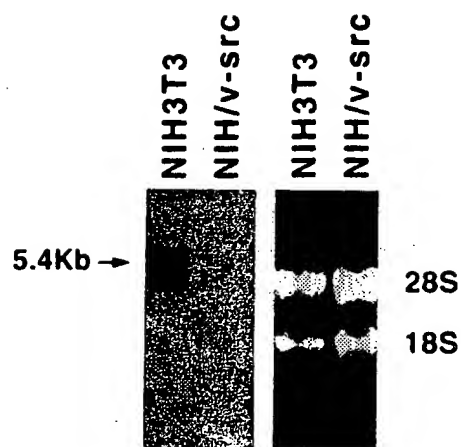


FIG.1

208040" 2E420650

203040 * 2E720550

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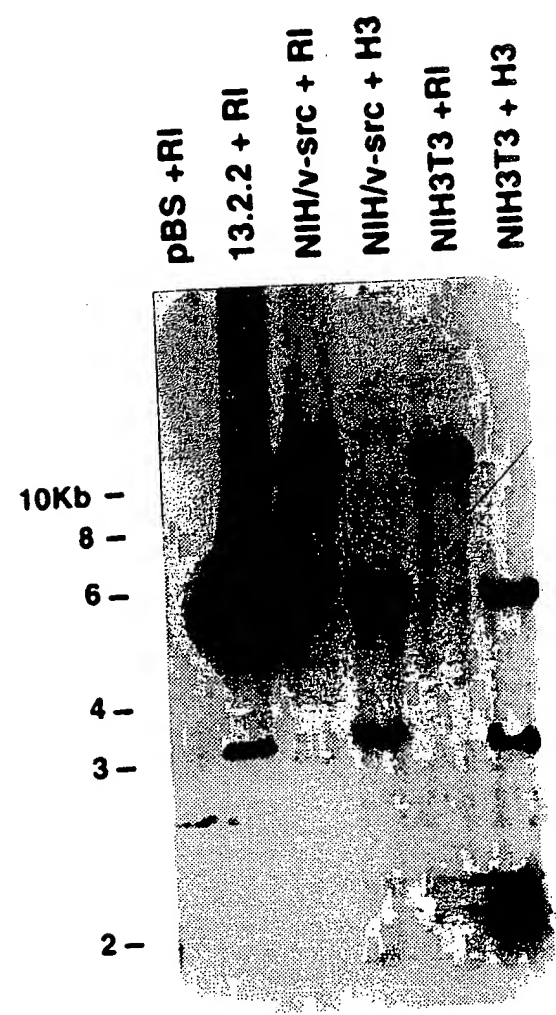


FIG.2A

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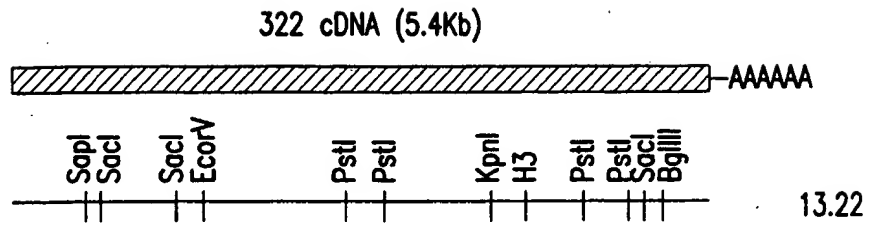


FIG.2B

208040* 2E420660

208040" 2E420650

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	ggaaaagacagagccagcctcggaggagcaggagccggcagaagacacagaccaggccag	60
	gttgtcagcagactacgagaaggtggagctgcctttggaagaccaggttggtgacctgga	120
	ggcatcgtcagaggagaagtgtgctcctttggcaacggaagtgttgatgagaagatgga	180
	M E	2
181	agcccaccaagaagttgttgcagaggtccacgtgagcaccgtggagaagacagaggagga	240
3	A H Q E V V A E V E V S T V E K T E E E	22
241	gcaggaggaggaggagaggctgaagggggcgtggtgtagaaggaacaggagaatcctt	300
23	Q G G G G E A E G G V V V E G T G E S L	42
301	gccccctgagaaactggctgagccccaggaggtccccaggaagctgagcctgctgagga	360
43	P P E K L A E P Q E V P Q E A E P A E E	62
361	gctgatgaagagcagagagatgtgtgtctctggaggagaccacactcaactgacagacct	420
63	L M K S R E M C V E G G D H T Q L T D L	82
421	aagtctgaagagaagacgctgccccaaacaccagaaggcattgtcagtgaggtggagat	480
83	S P E E K T L P K H P E G I V S E V E M	102
481	gctgtcctctcaggaaagaatcaaggtacagggaagtccttgaagaaactcttcagtag	540
103	L S S Q E R I K V Q G S P L K K L F S S	122
541	ctcaggcttaaagaagctgtctgggaagaagcagaaggggaaacgaggaggtgggggaga	600
123	S G L K K L S G K K Q K G K R G G G G D	142
601	cgaagagcctggagaataccaacacattcacaccgaatccccagagagtgtgatgagca	660
143	E E P G E Y Q H I H T E S P E S A D E Q	162

FIG.3A

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208040" 2E-120660

661	gaaggagagagctctgcgtcgtcccccaggagcctgaggagaccacgtgtctggagaa	720
163	K G E S S A S S P E E P E E T T C L E K	182
721	agggccgctggaagcaccagcatgggaagctgaggaaggaactacttcgtggagagaa	780
183	G P L E A P R M G K L R K E L L R G E <u>K</u>	202
781	gaagaggaaggatcactccctgggcatccttcaaaaagatggtgacaccaagaaacggt	840
203	<u>K R K</u> D H S L G I L Q K D G D T Q E T V	222
841	ccgaagaccttctgagagtgcagaaggagagctggagaaggtcaagagcgccacctt	900
223	R R P S E S D K E E E L E K V K S A T L	242
901	gtcctccactgatagcacagtgtcagaaatgcaagatgaagtcaaaactgttggtgagga	960
243	S S T D S T V S E M Q D E V K T V G E E	262
961	acaaaagccagaggaaccaaagcgtagggtggatacttcagtgtcttgggaagcactgat	1020
263	Q K P E E P K R R V D T S V S W E A L I	282
1021	ttgtgtcggatcatccaagaagagagcaaggaaggcatcctcttcagatataagagggcc	1080
283	C V G S S K <u>K R A R</u> K A S S S D I R G P	302
1081	aaggacactgggagggggacagtcacagagcagaggaggccagcaaagacaaagaagccg	1140
303	R T L <u>G G G Q S Q S R G G</u> Q Q R Q R S R	322
1141	aacagacgctgttctgccagcaccagcaggagcaggaccaagcgcaaggaagttcctcacc	1200
323	T D A V P A S T Q E Q D Q A Q G S S S P	342
1201	cgagccagcgggaagcccttccgaaggggaaggtgtctccacttgggagtcatttaaag	1260
343	E P A G S P S E G E G V S T W E S F K R	362

FIG.3B

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208040:2E720650

1261	attagtcactccaagaaaaaatccaagtcaaaactggaagagaaagaagccggaaggac	1320
363	L V T P R <u>K K S K</u> S K L E E K E A G R T	382
1321	tctagttgtaggagcaggttgtccactgagatcgaaccgtgtagagaagaatcttgggtt	1380
383	L V V G A G C P L R S N R V E K N L G F	402
1381	tccattaagaaattcatccccggacggcgaagaaaagggcagatgggaaggcaagaaca	1440
403	P L R N S S P D G G R K G Q M G R Q E Q	422
1441	agccactgtggaagactcagggccagtggagataaatgaggacgagcctgatgtcccagc	1500
423	A T V E D S G P V E I N E D E P D V P A	442
1501	agtcgtgcctctgtctgagtatgatgcagtggagaggagaagatggaagcccaggggaa	1560
443	V V P L S E Y D A V E R E K M E A Q G N	462
1561	tgcggagctgcccagctgctggggctgtgtagtgtccgaggagctcagtaagactctggt	1620
463	A E L P S C W G C V V S E E L S K T L V	482
1621	ccacactgtgagtgctgcagtcattgatgggaccagggcagtcaccagtgctgaagagcg	1680
483	H T V S V A V I D G T R A K T S K E E R	502
1681	gtctccttcgtggatatccgcttccgtaacagaacctcttgaacacacagcgggagaagc	1740
503	S P S W I S A S V T E P L E H T A G E A	522
1741	catgccacctgttgaagaggtcactgaaaaagacatcattgcagaagaaactcctgtgct	1800
523	M P P V E E V T E K D I I A E E T P V L	542
1801	cacccagacgttaccagagggtaagatgcccatgacgacatggtcaccagtgaagtgga	1860
543	T Q T L P E G K D A H D D M V T S E V D	562

FIG.3C

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090243 040802
208040 2E420660

1861	ttcacctcagaagctgtgacagccacagagacctcagaggtctccgtactgaagaagt	1920
563	F T S E A V T A T E T S E A L R T E E V	582
1921	taccgaagcatcggggccgaagagaccacagacatggtgtccgcagtttcccagctgac	1980
583	T E A S G A E E T T D M V S A V S Q L T	602
1981	tgactccccagacaccacagaggaagccacccagttcaggaggtagagggtggtgtgct	2040
603	D S P D T T E E A T P V Q E V E G G V L	622
2041	agatacagaagaagaggagcgcagacgcaggccatcctccaagccgttgacagacaaggt	2100
623	D T E E E E R Q T Q A I L Q A V A D K V	642
2101	gaaagaggagtcccaggtgcctgcaaccacagactgtgcagagaacggggtcaaaagcact	2160
643	K E E S Q V P A T Q T V Q R T G S K A L	662
2161	ggagaaggttgaggaggtagaggaggactccgaagtgtggttcggagaaagagaagga	2220
663	E K V E E V E E D S E V L A S E K E K D	682
2221	cgttatgccgaaaggacccgtgcaggaagctggagctgagcatcttgacagggctctga	2280
683	V M P K G P V Q E A G A E H L A Q G S E	702
2281	gactggacaggctactccagagagccttgaagttcctgaagtcacagcagatgtagacca	2340
703	T G Q A T P E S L E V P E V T A D V D H	722
2341	tgctgccacgtgccaggttatcaagctccagcagctgatggaacaggccgtggcccctga	2400
723	V A T C Q V I K L Q Q L M E Q A V A P E	742
2401	gtcatccgaaaccttgacagacagtgagacaaatggaagcactcccttagcagattcaga	2460
743	S S E T L T D S E T N G S T R L A D S D	762

FIG.3D

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09902432 040802

2461	cactgcagatgggacacagcaagatgaaaccattgacagccaggacagtaagccactgc	2520
763	T A D G T Q Q D E T I D S Q D S K A T A	782
2521	agctgtcaggcagtcacaggtcacagaagaagagcggtactgctcagaaaggagagcc	2580
783	A V E Q S Q V T E E E A A T A Q K E E P	802
2581	ttcgacactacctaataatgttccagcccaggaagaacatggggaagaaccaggaagaga	2640
803	S T L P N N V P A Q E E H G E E P G R D	822
2641	tgttcttgaacctacacagcaagagcttgctgctgcagccgtgccgtctggcaaaagac	2700
823	V L E P T Q Q E L A A A A V P V W Q K T	842
2701	tgaggtgggtcaagaggggtgaggttgactggttgatggagaaaaagtcaaagaagaaca	2760
843	E V G Q E G E V D W L D G E K V K E E Q	862
2761	ggaggtgtttgtacactctggacccaacagtcaaaaggctgctgatgtgacatatgacag	2820
863	E V F V H S G P N S Q K A A D V T Y D S	882
2821	tgaagtgatgggagtgccgggtgtcaggaaaaggagagtactgaagtgcagagtccttag	2880
883	E V M G V A G C Q E K E S T E V Q S L S	902
2882	cctggaggaggagagatggaaactgacgttgaaaaggagaaaaggagacaaagccaga	2940
903	L E E G E M E T D V E K E K R E T K P E	922
2941	gcaagtgagtgaagaaggtgagcaggaaacagccgctcctgagcatgaaaggaactacgg	3000
923	Q V S E E G E Q E T A A P E H E R N Y G	942
3001	gaagccagtcctgacacttgacatgcccagctcagagagggggaaggcactgggaagcct	3060
943	K P V L T L D M P S S E R G K A L G S L	962

FIG.3E

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208040" 2E420560

3061	tggaggaagcccttctctcccagaccaagacaaagcaggttgcatagaggttcaagttca	3120
963	G G S P S L P D Q D K A G C I E V Q V Q	982
3121	aagcctggacacaacagtcactcaaacagcagaagctgtgaaaaggtcatagaaacggt	3180
983	S L D T T V T Q T A E A V E K V I E T V	1002
3181	tgtgatttcagagacaggtgaaagtccagagtgtgtaggtgcacacttattaccagctga	3240
1003	V I S E T G E S P E Q V G A H L L P A E	1002
	→Zn-finger→	
3241	gaagtcctctgcaacgggtggccactggactcttcagcatgcagaggacacggtaccctt	3300
1023	K S S A T G G H W T L Q H A E D T V P L	1042
3301	ggggcctgagtcctcaggcagaatccatcccaatcatagtaactcctgctcctgaaagcac	3360
1043	G P E S Q A E S I P I I V T P A P E S T	1062
3361	cctacatcctgacctacaaggagaaataagcgcaccccagagagcgatcagaggaaga	3420
1063	L H P D L Q G E I S A S Q R E R S E E E	1082
3421	ggacaagccagatgctggtcctgatgctgacggcaaggagagtacagcaatcgacaaagt	3480
1083	D K P D A G P D A D G K E S T A I D K V	1102
3481	cctcaaggctgaacctgagatcctggaacttgagagtaagagcaacaagattgtgctgaa	3540
1103	L K A E P E I L E L E S K S N K I V L N	1122
3541	cgctattcagacagccgttgaccagttcgcacgtacagaaacagccccgaaactcatgc	3600
1123	V I Q T A V D Q F A R T E T A P E T H A	1142
3601	ttatgattcacagacccaggttcctgcaatgcgcttgacagcagggagcccaacagatg	3660
1143	Y D S Q T Q V P A M R L D S R E P N R C	1162

FIG.3F



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208040" 2E420660

3661	ctggacaaaaatgaaagttgccaagatgaaacacccagtgccgcagcccagagaggactt	3720
1163	W T K M K V A K M K H P V P Q P R E D L	1182
3721	gcaagtcctgaccgttctggaggcatggctcagctcgaaatgcttgccgcgcttgcaagt	3780
1183	Q V L T V L E A W L S S E M L A A L A V	1202
3781	tgaaagcgccggtgtcaaagtaagcattgagaagctgcctcctcaacccaaagatcaaaa	3840
1203	E S A G V K V S I E K L P P Q P K D Q K	1222
3841	ggagcatgctgctgatggccctcagctccaaagcttagcccaggcagaggcagtgctgg	3900
1223	E H A A D G P Q L Q S L A Q A E A V S G	1242
3901	aaacctaaccaaagaatccccagacaccaacggaccaaaagctaaccgaggagcgatgccc	3960
1243	N L T K E S P D T N G P K L T E E R C P	1262
3961	ccaaaagttgaggtccaggaagaagaatgtctaccaagtcagtc aaagagaacaaggcc	4020
1263	Q K L R S R K K K C L P S Q S K R T R P	1282
4021	caggcagaagaggacctgcaggagccaaagggagacctggcagaatcctaagatgttagt	4080
1283	R Q K R T C R S Q R E T W Q N P K M L V	1302
4081	tgctcattgtacatctgtaagaccagaatgtgaaaacaagtcacagaacaagatgctgct	4140
1303	A H C T S V R P E C E N K S Q N K M L L	1322
4141	gttgggaccttggaaccaagatttcagagcccatgagatccagagagcagggccgtccaat	4200
1323	L G P W T K I S E P M R S R E Q G R P M	1342
4201	gatttccaccagtagagcaccgccacaattctgaggcttcacgaggagctagagccagc	4260
1343	I S T Q *	1346

FIG.3G

203040" 2E420650



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4261	taacatttcctcggttcaagactgcctttgatttgccccttgatgccgtccgtgtatttc	4320
4321	ggatttaaggtcctgcgttctcaacctggaaccaattctgccatacctagttccacttct	4380
4381	caaaactggagcatcctcctttatgtatttatgtatgtttatgtagtcctcctcctgt	4440
4441	acctattgtatatttttttctaacgtttaagcacatgcttttgtattatgcaatatata	4500
4501	acgggtgtgcagccatagcgacgctttgaaaagctccaagcctcaactgtaacctgcagc	4560
4561	aaacagataacattcctggcaagaagagacaagtcttttttaagtttactgatgcttag	4620
4621	atctgtgggcttctagtcctctgaaagtgttgttttctatgcacagcgagctcagaaa	4680
4681	<u>t</u> aaaaccccatTTTgaaacatccaggatgtccaatattaccatgattttttccccct	4720
4721	ttttgctaattccagtcagggttggaagaagtcctcctgtgtcagattaagccctgtct	4780
4781	cttaatgatatggacaaatgagtggtgcctaaggccatgagatgttctaatgcagaagg	4840
4741	aatctgtgtacgtttttttgattgtactcttctatgctggaccgaattcatatgcagat	4900
4901	cgaagtgagtcctgttctttacagatggtatTTTgataactggagtttgtctgtgtt	4960
4961	atatctgtgcccttctTTTaaacaatgttgcattatgttcctttggataaattgtgat	5020
5021	ttgacaactgatttaaa <u>t</u> aaacatatttgactac(A).	

FIG.3H

208040" 2E420660

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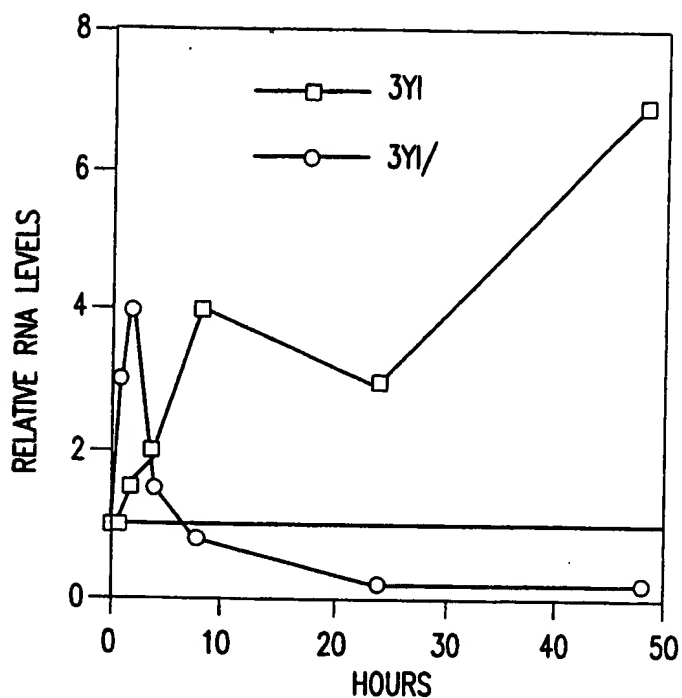


FIG.4A

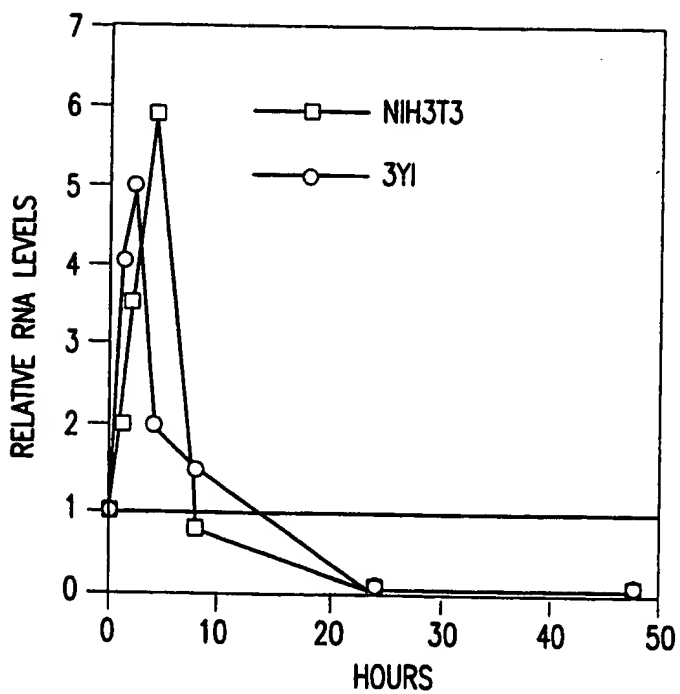


FIG.4B

208040" 2E420660

(13 of



rat-6/mos
rat-6/src
rat-6/myc
rat-6/neu
rat-6/ras
rat-6/raf-1
rat-6



FIG.5



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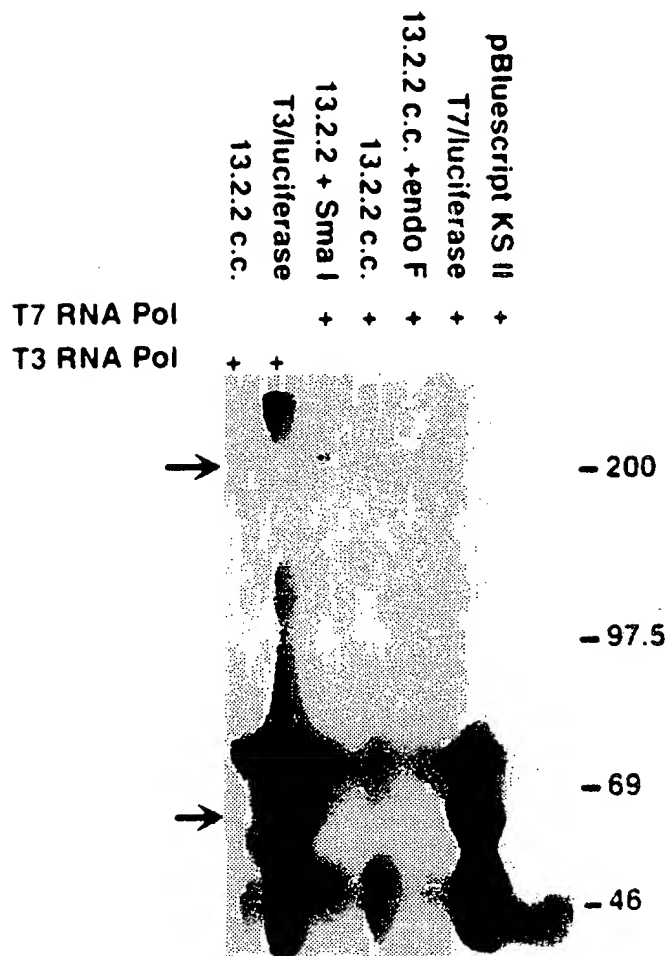


FIG.6

09902432.040802

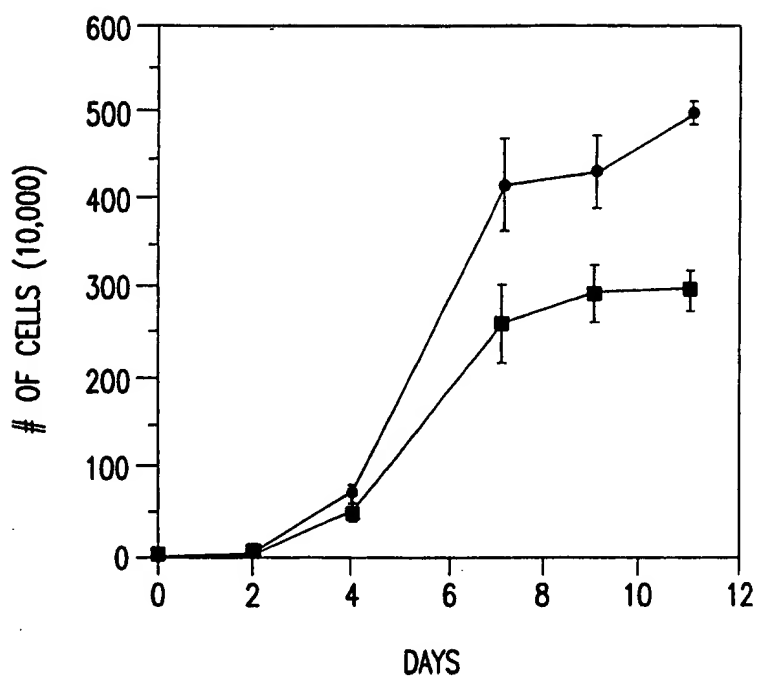


FIG.7A

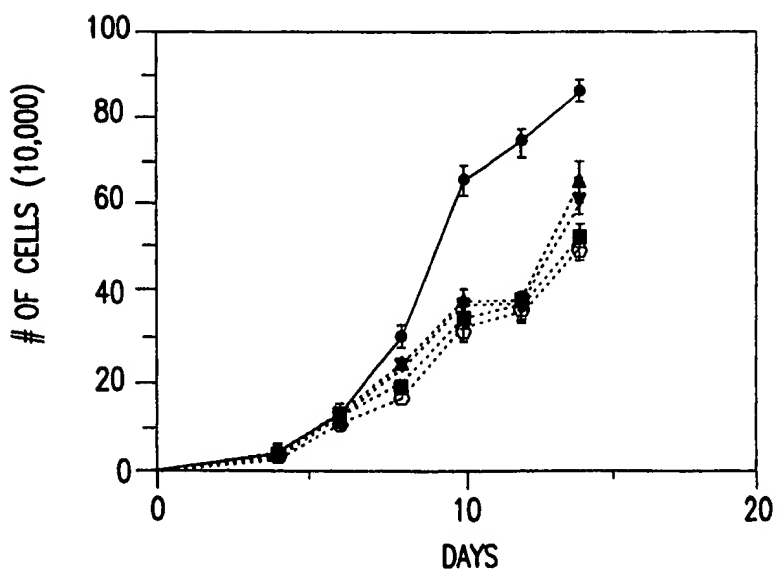


FIG.7B

208040" 2E420660

208040" 2E420660

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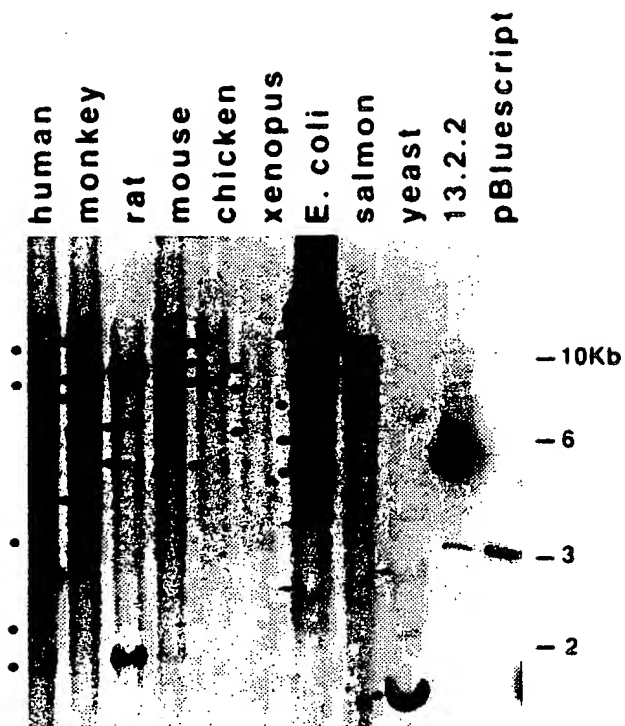


FIG.8

208040" 2E420660

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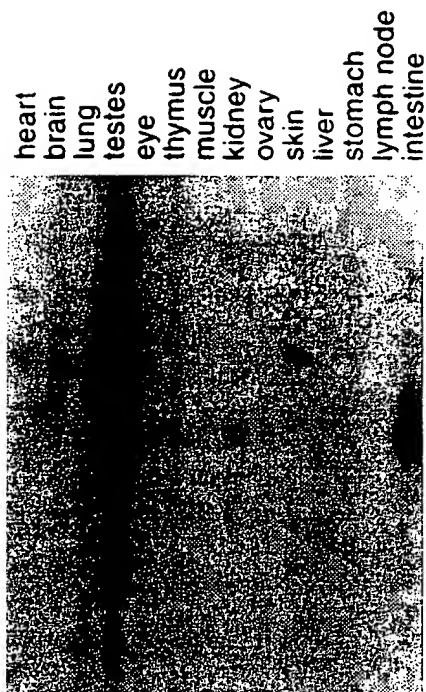


FIG.9

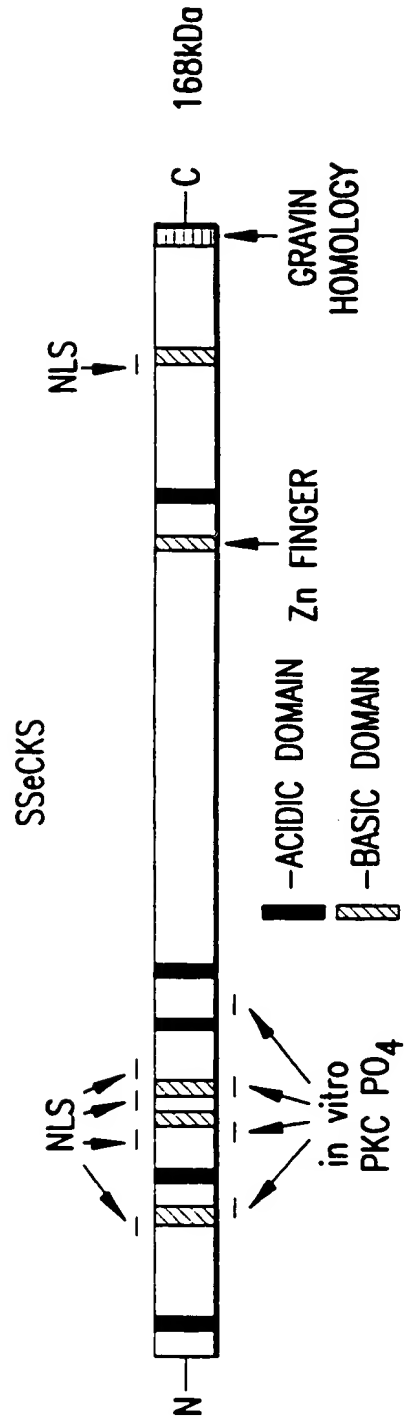


FIG.10

209040" 25420650



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5'	ATG	GGC	GCA	GGC	AGT	TCC	ACC	GAG	CAG	CGG	AGC	CCC	GAG	CAG	CCG	GCG	GGG	AGC
	M	G	A	G	S	S	T	E	Q	R	S	P	E	Q	P	A	G	S
	GAC	ACG	CCG	AGC	GAG	CTG	GTG	CTC	AGT	GGC	CAT	GGG	CCC	GCA	GCT	GAA	GCC	TCG
	D	T	P	S	E	L	V	L	S	G	H	G	P	A	A	E	A	S
	GGA	GCA	GCT	GGA	GAC	CCC	GCC	GAC	GCG	GAC	CCC	GCC	ACC	AAG	CTC	CCA	CAG	AAG
	G	A	A	G	D	P	A	D	A	D	P	A	T	K	L	P	Q	K
	AAT	GGC	CAG	CTG	TCT	TCT	GTC	AAC	GGC	GTA	GCT	GAA	CAA	GGA	GAT	GTC	CAT	GTC
	N	G	Q	L	S	S	V	N	G	V	A	E	Q	G	D	V	H	V
	CAA	GAG	GAA	AAC	CAG	GAG	GGG	CAG	GAG	GAA	GAA	GTC	GTT	GAT	GAG	GAT	GTT	GGA
	Q	E	E	N	Q	E	G	Q	E	E	E	V	V	D	E	D	V	G
	CAG	CGA	GAG	TCA	GAA	GAT	GTG	AGA	GAA	AAA	GAC	CGA	GTT	GAA	GAA	ATG	GCG	GCC
	Q	R	E	S	E	D	V	R	E	K	D	R	V	E	E	M	A	A
	AAC	TCC	ACA	GCT	GTT	GAA	GAT	ATC	ACA	AAG	GAT	GGG	CAG	GAG	GAG	ACA	TCA	GAA
	N	S	T	A	V	E	D	I	T	K	D	G	Q	E	E	T	S	E
	ATA	ATT	GAA	CAG	ATC	CCT	GCT	TCA	GAA	AAC	AAT	GTG	GAA	GAA	ATG	GTA	CAG	CCT
	I	I	E	Q	I	P	A	S	E	N	N	V	E	E	M	V	Q	P

FIG.11A

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441	450	459	468	477	486
GCT GAG TCC CAG GCT AAT GAT GTT GGC TTC AAG AAA GTA TTT AAA TTT GTT GGT					
A E S Q A N D V G F K K V F K F V G					
495	504	513	522	531	540
TTT AAA TTC ACG GTG AAG AAG GAT AAA AAT GAA AAG TCA GAT ACT GTC CAA CTA					
F K F T V K K D K N E K S D T V Q L					
549	558	567	576	585	594
CTC ACT GTC AAG AAG GAT GAA GGC GAA GGG GCA GAA GCC TCT GTC GGA GCT GGA					
L T V K K D E G E G A E A S V G A G					
603	612	621	630	639	648
GAC CAC CAG GAG CCC AGT GTG GAG ACT GCC GTC GGA GAG TCA GCA TCC AAA GAA					
D H Q E P S V E T A V G E S A S K E					
657	666	675	684	693	702
AGT GAG CTG AAG CAA TCC ACA GAG AAG CAA GAA GGC ACC CTG AAG CAA GAA CAG					
S E L K Q S T E K Q E G T L K Q E Q					
711	720	729	738	747	756
AGC AGC ACA GAA ATC CCC CTT CAA GCC GAA TCT GAT CAA GCG GCT GAG GAA GAA					
S S T E I P L Q A E S D Q A A E E E					
765	774	783	792	801	810
GCC AAA GAT GAA GGA GAA GAA AAA CAA GAG AAA GAG CCC ACC AAG TCC CCA GAA					
A K D E G E E K Q E K E P T K S P E					
819	828	837	846	855	864
TCC CCG AGC AGC CCA GTC AAC AGT GAG ACA ACA TCT TCC TTC AAG AAG TTC TTC					
S P S S P V N S E T T S S F K K F F					

FIG.11B



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873 882 891 900 909 918
ACT CAC GGT TGG GCC GGC TGG CGC AAG AAG ACC AGC TTC AAG AAA TCA AAA GAG

T H G W A G W R K K T S F K K S K E

927 936 945 954 963 972
GAT GAT CTG GAA ACT GCC GAG AAG AGA AAG GAG CAA GAG GCA GAA AAA GTA GAC

D D L E T A E K R K E Q E A E K V D

981 990 999 1008 1017 1026
GAG GAA GAA AAG GAA AAG ACA GAG CCA GCC TCG GAG GAG CAG GAG CCG GCA GAA

E E E K E K T E P A S E E Q E P A E

1035 1044 1053 1062 1071 1080
GAC ACA GAC CAG GCC AGG TTG TCA GCA GAC TAC GAG AAG GTG GAG CTG CCT TTG

D T D Q A R L S A D Y E K V E L P L

1089 1098 1107 1116 1125 1134
GAA GAC CAG GTT GGT GAC CTG GAG GCA TCG TCA GAG GAG AAG TGT GCT CCT TTG

E D Q V G D L E A S S E E K C A P L

1143 1152 1161 1170 1179 1188
GCA ACG GAA GTG TTT GAT GAG AAG ATG GAA GCC CAC CAA GAA GTT GTT GCA GAG

A T E V F D E K M E A H Q E V V A E

1197 1206 1215 1224 1233 1242
GTC CAC GTG AGC ACC GTG GAG AAG ACA GAG GAG GAG CAG GGA GGA GGA GGA GAG

V H V S T V E K T E E E Q G G G G E

1251 1260 1269 1278 1287 1296
GCT GAA GGG GGC GTG GTG GTA GAA GGA ACA GGA GAA TCC TTG CCC CCT GAG AAA

A E G G V V V E G T G E S L P P E K

FIG.11C

208040" 2E+20650



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1305	1314	1323	1332	1341	1350
CTG GCT GAG CCC CAG GAG GTC CCC CAG GAA GCT GAG CCT GCT GAG GAG CTG ATG					
L A E P Q E V P Q E A E P A E E L M					
1359	1368	1377	1386	1395	1404
AAG AGC AGA GAG ATG TGT GTC TCT GGA GGA GAC CAC ACT CAA CTG ACA GAC CTA					
K S R E M C V S G G D H T Q L T D L					
1413	1422	1431	1440	1449	1458
AGT CCT GAA GAG AAG ACG CTG CCC AAA CAC CCA GAA GGC ATT GTC AGT GAG GTG					
S P E E K T L P K H P E G I V S E V					
1467	1476	1485	1494	1503	1512
GAG ATG CTG TCC TCT CAG GAA AGA ATC AAG GTA CAG GGA AGT CCC TTG AAG AAA					
E M L S S Q E R I K V Q G S P L K K					
1521	1530	1539	1548	1557	1566
CTC TTC AGT AGC TCA GGC TTA AAG AAG CTG TCT GGG AAG AAG CAG AAG GGG AAA					
L F S S S G L K K L S G K K Q K G K					
1575	1584	1593	1602	1611	1620
CGA GGA GGT GGG GGA GAC GAA GAG CCT GGA GAA TAC CAA CAC ATT CAC ACC GAA					
R G G G G D E E P G E Y Q H I H T E					
1629	1638	1647	1656	1665	1674
TCC CCA GAG AGT GCT GAT GAG CAG AAG GGA GAG AGC TCT GCG TCG TCC CCC GAG					
S P E S A D E Q K G E S S A S S P E					
1683	1692	1701	1710	1719	1728
GAG CCT GAG GAG ACC ACG TGT CTG GAG AAA GGG CCG CTG GAA GCA CCC CAG GAT					
E P E E T T C L E K G P L E A P Q D					

FIG.11D

209040" 2E420660



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1737	1746	1755	1764	1773	1782
GGG GAA GCT GAG GAA GGA ACT ACT TCC GAT GGA GAG AAG AAG AGA GAA GGG ATC					
G E A E E G T T S D G E K K R E G I					
1791	1800	1809	1818	1827	1836
ACT CCC TGG GCA TCC TTC AAA AAG ATG GTG ACA CCC AAG AAA CGG GTC CGA AGA					
T P W A S F K K M V T P K K R V R R					
1845	1854	1863	1872	1881	1890
CCT TCT GAG AGT GAC AAG GAG GAA GAG CTG GAG AAG GTC AAG AGC GCC ACC TTG					
P S F S D K E E E L E K V K S A T L					
1899	1908	1917	1926	1935	1944
TCC TCC ACT GAT AGC ACA GTG TCA GAA ATG CAA GAT GAA GTC AAA ACT GTT GGT					
S S T D S T V S E M Q D E V K T V G					
1953	1962	1971	1980	1589	1998
GAG GAA CAA AAG CCA GAG GAA CCA AAG CGT AGG GTG GAT ACT TCA GTG TCT TGG					
E E Q K P E E P K R R V D T S V S W					
2007	2016	2025	2034	2043	2052
GAA GCA CTG ATT TGT GTC GGA TCA TCC AAG AAG AGA GCA AGG AAG GCA TCC TCT					
E A L I C V G S S K K R A R K A S S					
2061	2070	2079	2088	2097	2106
TCA GAT GAT GAA GGA GGG CCA AGG ACA CTG GGA GGG GAC AGT CAC AGA GCA GAG					
S D D E G G P R T L G G D S H R A E					
2115	2124	2133	2142	2151	2160
GAG GCC AGC AAA GAC AAA GAA GCC GGA ACA GAC GCT GTT CCT GCC AGC ACC CAG					
E A S K D K E A G T D A V P A S T Q					

FIG.11E

09902432 040802



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2169 2178 2187 2196 2205 2114
GAG CAG GAC CAA GCG CAA GGA AGT TCC TCA CCC GAG CCA GCG GGA AGC CTT TCC
E Q D Q A Q G S S S P E P A G S P S

2223 2232 2241 2250 2259 2268
GAA GGG GAA GGT GTC TCC ACT TGG GAG TCA TTT AAA AGA TTA GTC ACT CCA AGA
E G E G V S T W E S F K R L V T P R

2277 2286 2295 2304 2313 2322
AAA AAA TCC AAG TCA AAA CTG GAA GAG AAA GCC GAA GAC TCT AGT GTA GAG CAG
K K S K S K L E E K A E D S S V E Q

2331 2340 2349 2358 2367 2376
TTG TCC ACT GAG ATC GAA CCG AGT AGA GAA GAA TCT TGG GTT TCC ATT AAG AAA
L S T E I E P S R E E S W V S I K K

2385 2394 2403 2412 2421 2430
TTC ATC CCC GGA CGG CGG AAG AAA AGG GCA GAC GGG AAG CAA GAA CAA GCC ACT
F I P G R R K K R A D G K Q E Q A T

2439 2448 2457 2466 2475 2484
GTG GAA GAC TCA GGG CCA GTG GAG ATA AAT GAG GAC GAC CCT AAT GTC CCA GCC
V E D S G P V E I N E D D P N V P A

2493 2502 2511 2520 2529 2538
GTC GTG CCT CTG TCT GAG TAT AAT GCA GTG GAG AGG GAG AAG ATG GAA GCC CAG
V V P L S E Y N A V E R E K M E A Q

2547 2556 2565 2574 2583 2592
GGG AAT ACG GAG CTG CCC CAG CTG CTG GGG GCT GTG TAC GTG TCC GAG GAG CTC
G N T E L P Q L L G A V Y V S E E L

FIG.11F

208040 23420550

208040" 2E+20660



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2601	2610	2619	2628	2637	2646
AGT AAG ACT CTG GTC CAC	ACT GTG AGT GTC GCA GTC	ATT GAT GGG ACC AGG GCA			

S K T L V H T V S V A V I D G T R A					

2655	2664	2673	2682	2691	2700
GTC ACC AGT GTC GAA GAG CGG TCT CCT TCG TGG ATA TCC GCT TCC GTA ACA GAA					

V T S V E E R S P S W I S A S V T E					

2790	2718	2727	2736	2745	2754
CCT CTT GAA CAC ACA GCG GGA GAA GCC ATG CCA CCT GTT GAA GAG GTC ACT GAA					

P L E H T A G E A M P P V E E V T E					

2763	2772	2781	2790	2799	2808
AAA GAC ATC ATT GCA GAA GAA ACT CCT GTG CTC ACC CAG ACG TTA CCA GAG GGT					

K D I I A E E T P V L T Q T L P E G					

2817	2826	2835	2844	2853	2862
AAA GAT GCC CAT GAC GAC ATG GTC ACC AGT GAA GTG GAT TTC ACC TCA GAA GCT					

K D A H D D M V T S E V D F T S E A					

2871	2880	2889	2898	2907	2916
GTG ACA GCC ACA GAG ACC TCA GAG GCT CTC CGT ACT GAA GAA GTT ACC GAA GCA					

V T A T E T S E A L R T E E V T E A					

2925	2934	2943	2952	2961	2970
TCG GGG GCC GAA GAG ACC ACA GAC ATG GTG TCC GCA GTT TCC CAG CTG ACT GAC					

S G A E E T T D M V S A V S Q L T D					

2979	2988	2997	3006	3015	3024
TCC CCA GAC ACC ACA GAG GAA GCC ACC CCA GTT CAG GAG GTA GAG AGT GGT GTG					

S P D T T E E A T P V Q E V E S G V					

FIG.11G

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3033 3042 3051 3060 3069 3078
CTA GAT ACA GAA GAA GAG GAG CGC CAG ACG CAG GCC ATC CTC CAA GCC GTT GCA

L D T E E E E R Q T Q A I L Q A V A

3087 3096 3105 3114 3123 3132
GAC AAG GTG AAA GAG GAG TCC CAG GTG CCT GCA ACC CAG ACT GTG CAG AGA ACG

D K V K E E S Q V P A T Q T V Q R T

3141 3150 3159 3168 3177 3186
GGG TCA AAA GCA CTG GAG AAG GTT GAG GAG GTA GAG GAG GAC TCC GAA GTG CTG

G S K A L E K V E E V E E D S E V L

3195 3204 3213 3222 3231 3240
GCT TCG GAG AAA GAG AAG GAC GTT ATG CCG AAA GGA CCC GTG CAG GAA GCT GGA

A S E K E K D V M P K G P V Q E A G

3195 3258 3267 3276 3285 3294
GCT GAG CAT CTT GCA CAG GGC TCT GAG ACT GGA CAG GCT ACT CCA GAG AGC CTT

A E H L A Q G S E T G Q A T P E S L

3303 3312 3321 3330 3339 3348
GAA GTT CCT GAA GTC ACG GCA GAT GTA GAC CAT GTC GCC ACG TGC CAG GTT ATC

E V P E V T A D V D H V A T C Q V I

3357 3366 3375 3384 3393 3402
AAG CTC CAG CAG CTG ATG GAA CAG GCC GTG GCC CCT GAG TCA TCC GAA ACC TTG

K L Q Q L M E Q A V A P E S S E T L

3411 3420 3429 3438 3447 3456
ACA GAC AGT GAG ACA AAT GGA AGC ACT CCC TTA GCA GAT TCA GAC ACT GCA GAT

T D S E T N G S T P L A D S D T A D

FIG.1 1H

208040" 2E+20660

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3465 3474 3483 3492 3501 3510
GGG ACA CAG CAA GAT GAA ACC ATT GAC AGC CAG GAC AGT AAA GCC ACT GCA GCT

G T Q Q D E T I D S Q D S K A T A A

3519 3528 3537 3546 3555 3564
GTC AGG CAG TCA CAG GTC ACA GAA GAA GAG GCG GCT ACT GCT CAG AAA GAG GAG

V R Q S Q V T E E E A A T A Q K E E

3573 3582 3591 3600 3609 3618
CCT TCG ACA CTA CCT AAT AAT GTT CCA GCC CAG GAA GAA CAT GGG GAA GAA CCA

P S T L P N N V P A Q E E H G E E P

3627 3636 3645 3654 3663 3672
GGA AGA GAT GTT CTT GAA CCT ACA CAG CAA GAG CTT ACT GCT GCA GCC GTG CCC

G R D V L E P T Q Q E L T A A A V P

3681 3690 3699 3708 3717 3726
GTT CTG GCA AAG ACT GAG GTG GGT CAA GAG GGT GAG GTT GAC TGG TTG GAT GGA

V L A K T E V G Q E G E V D W L D G

3735 3744 3753 3762 3771 3780
GAA AAA GTC AAA GAA GAA CAG GAG GTG TTT GTA CAC TCT GGA CCC AAC AGT CAA

E K V K E E Q E V F V H S G P N S Q

3789 3798 3807 3816 3825 3834
AAG GCT GCT GAT GTG ACA TAT GAC AGT GAA GTG ATG GGA GTG GCC GGG TGT CAG

K A A D V T Y D S E V M G V A G C Q

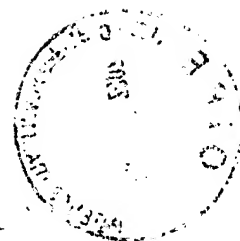
3843 3852 3861 3870 3879 3888
GAA AAG GAG AGT ACT GAA GTG CAG AGT CTT AGC CTG GAG GAG GGA GAG ATG GAA

E K E S T E V Q S L S L E E G E M E

FIG.111

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3897 3906 3915 3924 3933 3942
ACT GAC GTT GAA AAG GAG AAA AGG GAG ACA AAG CCA GAG CAA GTG AGT GAA GAA

T D V E K E K R E T K P E Q V S E E

3951 3960 3969 3978 3987 3996
GGT GAG CAG GAA ACA GCC GCT CCT GAG CAT GAA GGA ACC TAC GGG AAG CCA GTC

G E Q E T A A P E H E G T Y G K P V

4005 4014 4023 4032 4041 4050
CTG ACA CTT GAC ATG CCC AGC TCA GAG AGG GGG AAG GCA CTG GGA AGC CTT GGA

L T L D M P S S E R G K A L G S L G

4059 4068 4077 4086 4095 4104
GGA AGC CCT TCT CTC CCA GAC CAA GAC AAA GCA GGT TGC ATA GAG GTT CAA GTT

G S P S L P D Q D K A G C I E V Q V

4113 4122 4131 4140 4149 4158
CAA AGC CTG GAC ACA ACA GTC ACT CAA ACA GCA GAA GCT GTG GAA AAG GTC ATA

Q S L D T T V T Q T A E A V E K V I

4167 4176 4185 4194 4203 4212
GAA ACG GTT GTG ATT TCA GAG ACA GGT GAA AGT CCA GAG TGT GTA GGT GAC CAC

E T V V I S E T G E S P E C V G A H

4221 4230 4239 4248 4257 4266
TTA TTA CCA GCT GAG AAG TCC TCT GCA ACG GGT GGC CAC TGG ACT CTT CAG CAT

L L P A E K S S A T G G H W T L Q H

4275 4284 4293 4902 4311 4320
GCA GAG GAC ACG GTA CCC CTG GGG CCT GAG TCT CAG GCA GAA TCC ATC CCA ATC

A E D T V P L G P E S Q A E S I P I

FIG.11J

208010.2E120650

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4329 4338 4347 4356 4365 4374
ATA GTA ACT CCT GCT CCT GAA AGC ACC CTA CAT CCT GAC CTA CAA GGA GAA ATA

I V T P A P E S T L H P D L Q G E I

4383 4392 4401 4410 4419 4428
AGC GCA TCC CAG AGA GAG CGA TCA GAG GAA GAG GAC AAG CCA GAT GCT GGT CCT

S A S Q R E R S E E E D K P D A G P

4437 4446 4455 4464 4473 4482
GAT GCT GAC GGC AAG GAG AGT ACA GCA ATC GAA AAA GTC CTC AAG GCT GAA CCT

D A D G K E S T A I E K V L K A E P

4491 4500 4509 4518 4527 4536
GAG ATC CTG GAA CTT GAG AGT AAG AGC AAC AAG ATT GTG CTG AAC GTC ATT CAG

E I L E L E S K S N K I V L N V I Q

4545 4554 4563 4572 4581 4590
ACA GCC GTT GAC CAG TTC GCA CGT ACA GAA ACA GCC CCC GAA ACT CAT GCT TAT

T A V D Q F A R T E T A P E T H A Y

4599 4608 4617 4626 4635 4644
GAT TCA CAG ACC CAG GTT CCT GCA TGC AGG CTT GAC AGC AGG GAG CCC AAC AGA

D S Q T Q V P A C R L D S R E P N R

4653 4662 4671 4680 4689 4698
TGC TGG ACA AAA ATG AAA GAT GCC AAG ATG AAA CAC CCA GTG CCG CAG CCC AGA

C W T K M K D A K M K H P V P Q P R

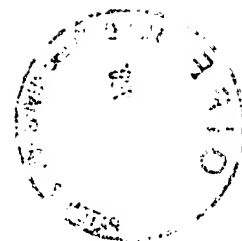
4707 4716 4725 4734 4743 4752
GAG GAC TTG CAA GTC CTG ACC GTT CTG GAG GCA TGG GCT CAG CCT CGG AAA TGC

E D L Q V L T V L E A W A Q P R K C

FIG.11K

208040" 2E420550

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4761 4770 4779 4788 4797 4806
TTG CCG CGC TTG CAG TTG AAA GCG CCG GTG TCA AAG TAA GCA TTG AGA AGC TGC

L P R L Q L K A P V S K *

4815 4824 4833 4842 4851 4860
CTC CTC AAC CCA AAG ATC CAA AAG GAG CAT GCT GCT GAT GGC CCT CAG CTC CAA

4869 4878 4887 4896 4905 4914
AGC TTA GCC CAG GCA GAG GCC AGT GCC TCT GGA AAC CTA ACC AAA GAA TCC CCA

4923 4932 4941 4950 4959 4968
GAC ACC ACC GGA CCA AAG CTA ACC GAG GAG GGC GAT CCC CCA AAA GTT CAG GTC

4977 4986 4995 5004 5013 5022
CAG GAA GAA GAA ATG TCT ACC AAG TCA GTC AAA GAG AAC AAG GCC CAG GCA GAA

5031 5040 5049 5058 5067 5076
GAG GAC CTG CAG GAG CCA AAG GGA GAC CTG GCA GAA TCC TCC GAT GTT AGT TGC

5085 5094 5103 5112 5121 5130
TCA TTG TAC ATC TGT AAG ACC AGA ATG TGA AAA CAA GTC ACA GAA CAA GAT GCT

5139 5148 5157 5166 5175 5184
GCT GTT GGG ACC TTG AGA CCA AGA TTT CAG AGC CCA TGA CAT CCA GAG AGC AGG

5193
GCC GTC CAA TGA TTT C 3'

FIG.11L

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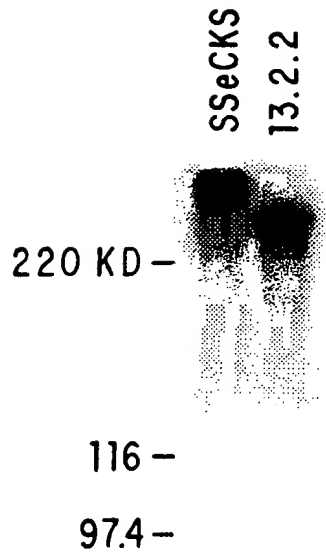


FIG.12

208040" 2E720660

203040" 2E-420650

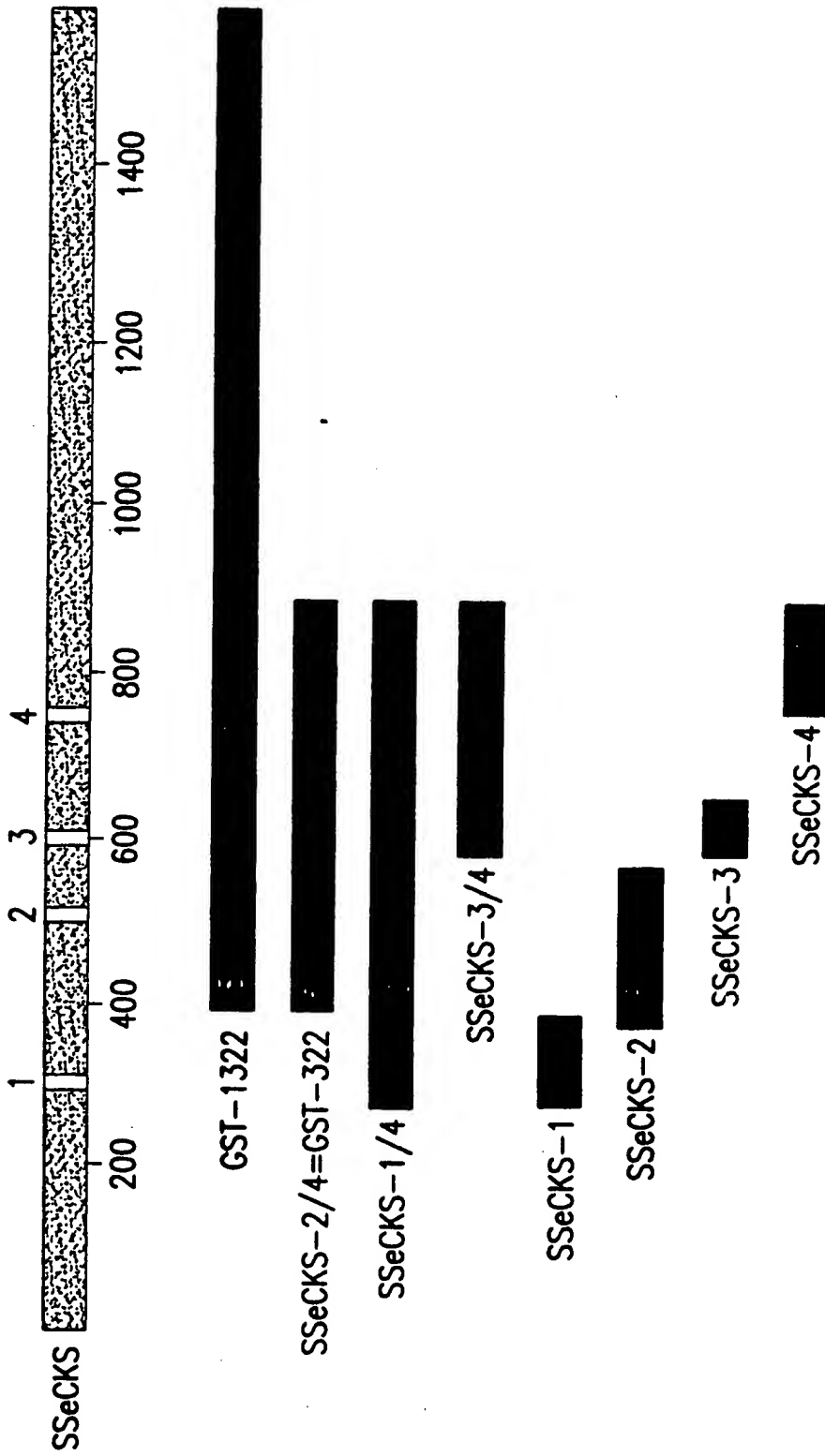


FIG.13A

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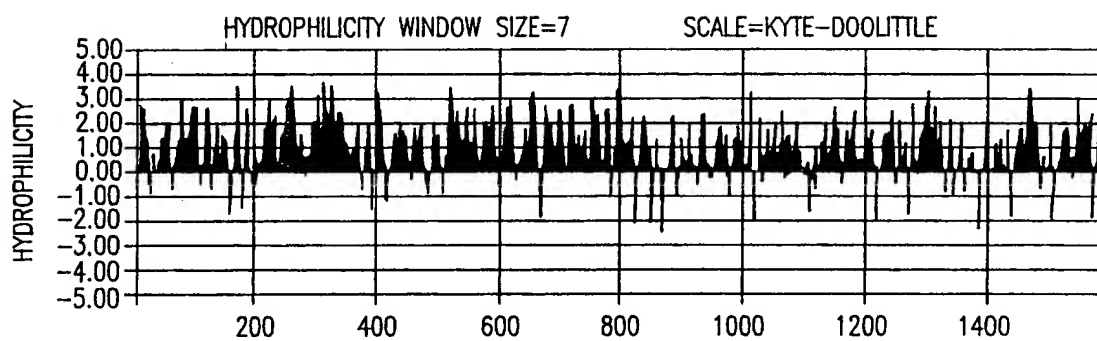
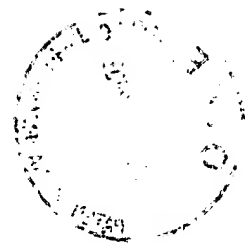


FIG.13B

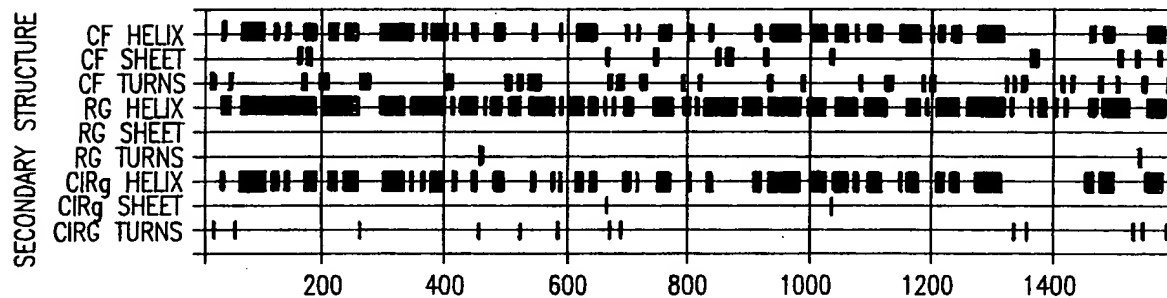


FIG.13C

208040"2E+20660

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PMA	0	2'	10'	10'
Inhibitor	-	-	-	+

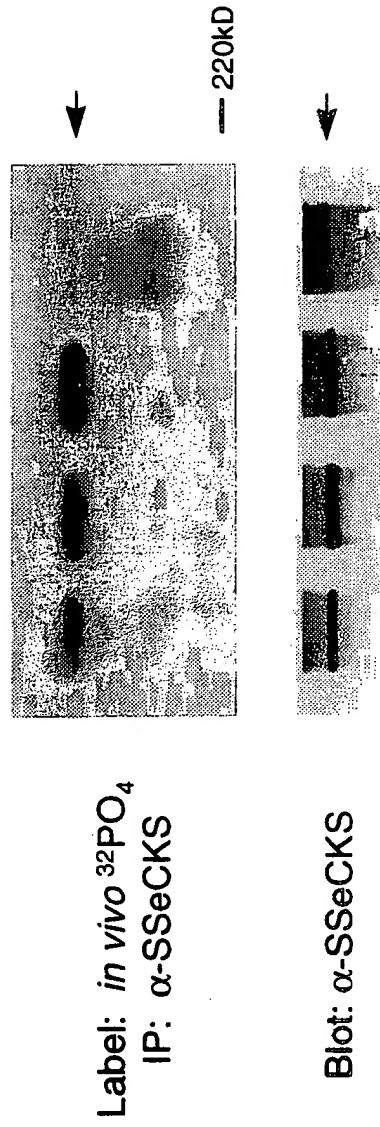


FIG.14



208040" 2E720660

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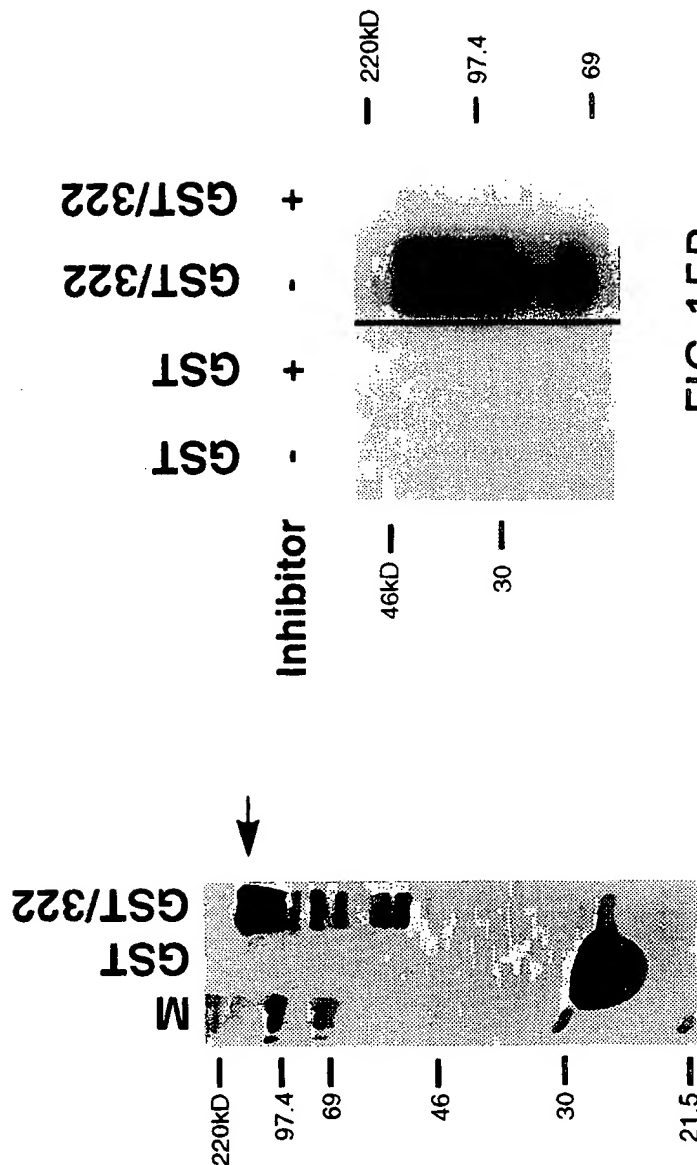
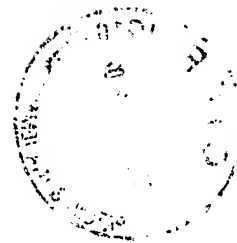


FIG.15B

FIG.15A

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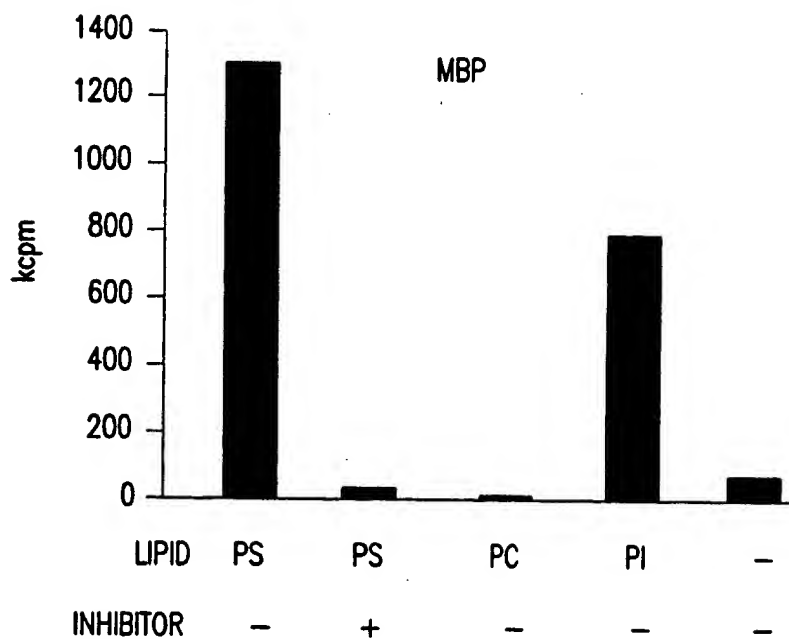


FIG.16A

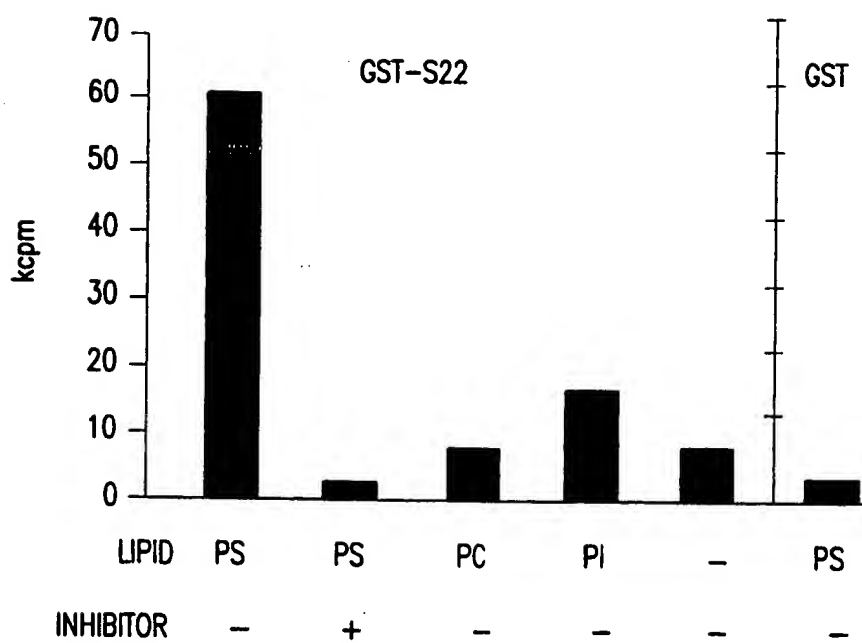


FIG.16B

208040" 2E720550

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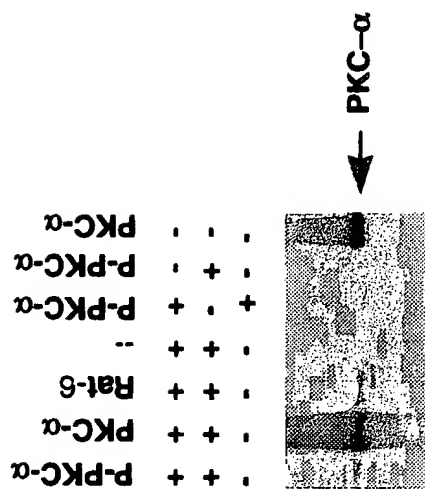
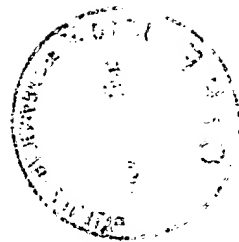


FIG.17B

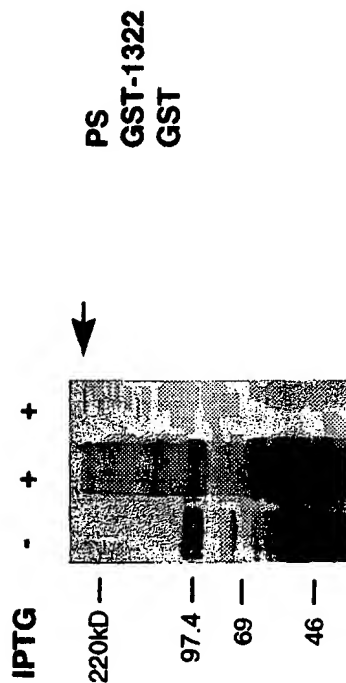


FIG.17A

208040"23420550

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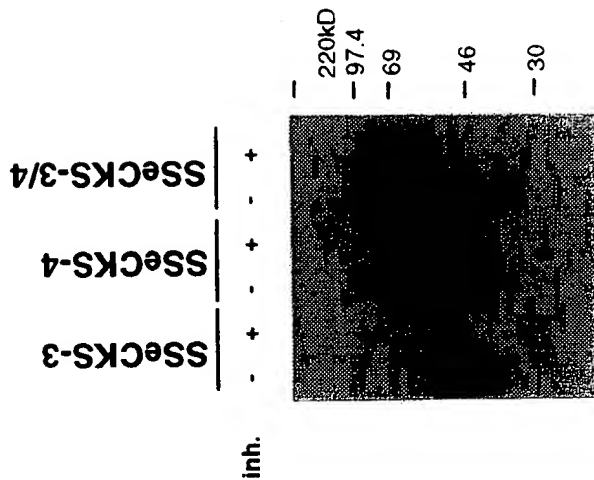


FIG.18B

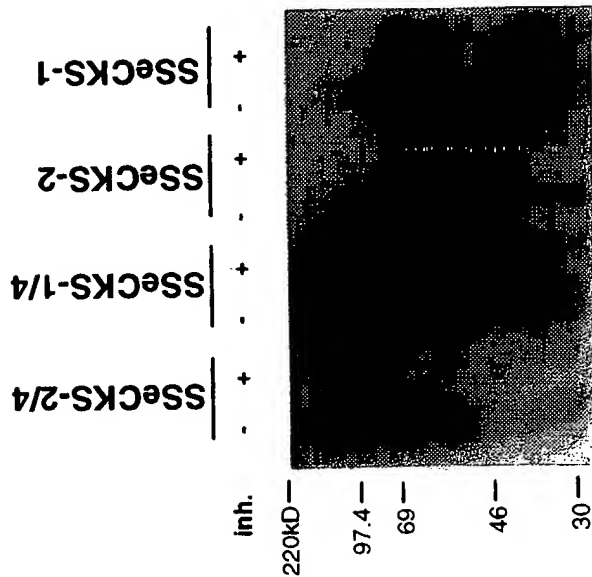
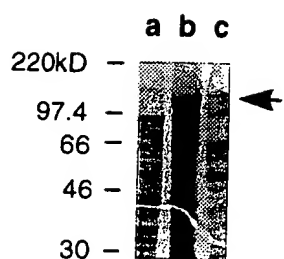
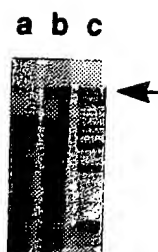


FIG.18A

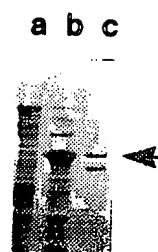
(39 of 90)



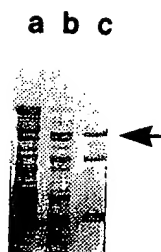
SSeCKS-2/4
FIG.18C



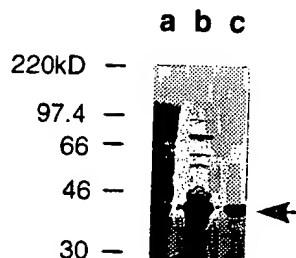
SSeCKS-1/4
FIG.18D



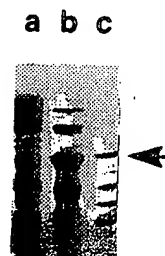
SSeCKS-2
FIG.18E



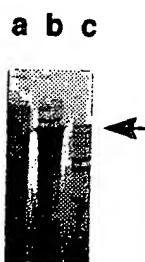
SSeCKS-1
FIG.18F



SSeCKS-3
FIG.18G



SSeCKS-4
FIG.18H



SSeCKS-3/4
FIG.18I

202070" 2E+20660

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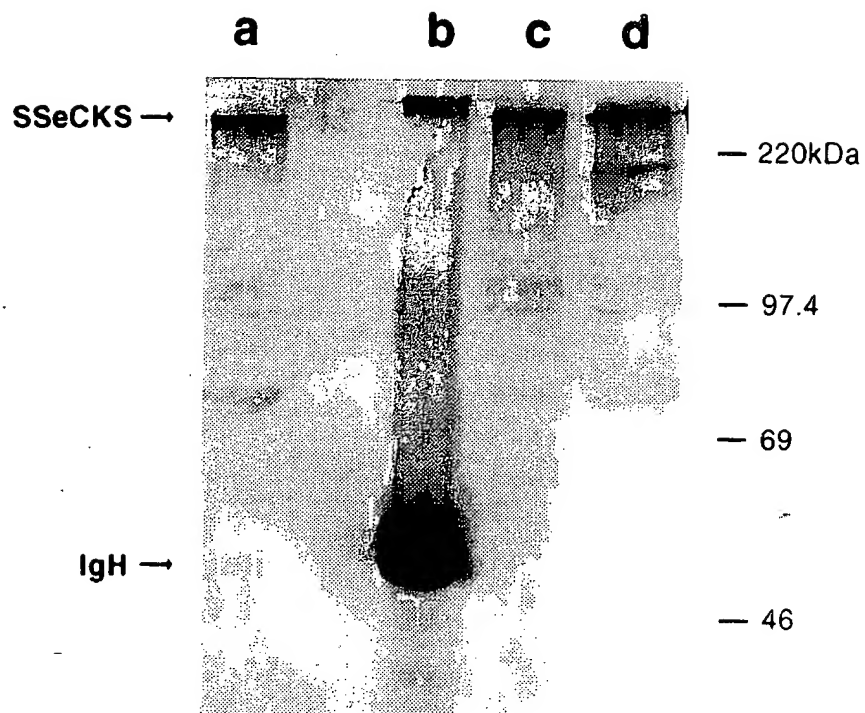


FIG.19

202040, 2E420660

208040" 2E420650

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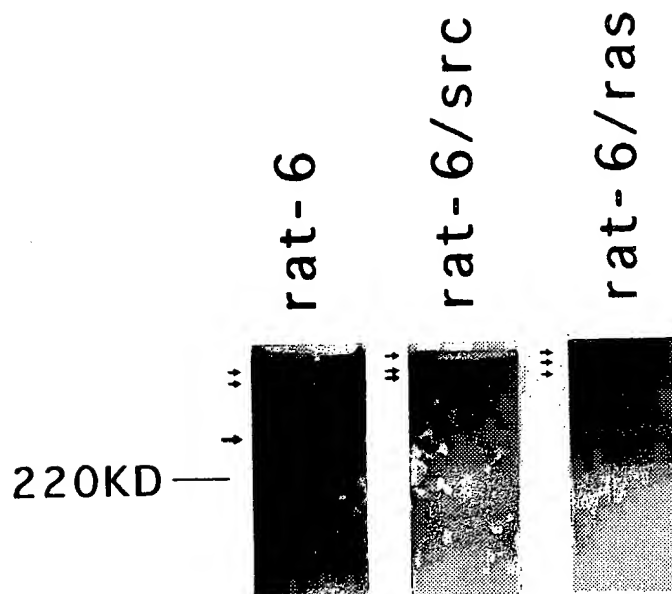


FIG.20

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FIG.21A



FIG.21B



FIG.21C



FIG.21D



FIG.21E



FIG.21F



FIG.21G



FIG.21H



FIG.21I

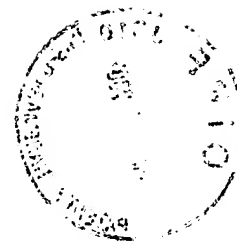


FIG.21J

208040-2E420650

208040" 2E420650

(43 f 10)



Rat-6/PKC α Rat-6

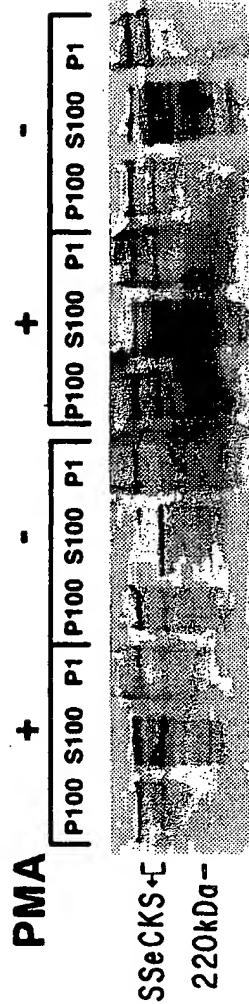


FIG.22

209040" 2E420660

(44 8 90)



spleen
thymus
prostate
testes
ovary
small intestine
colon
PBL

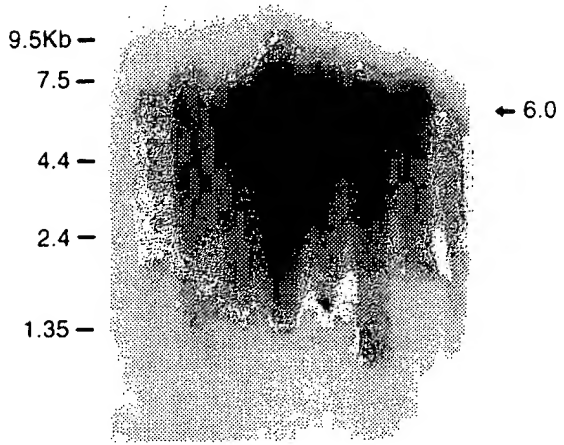


FIG.23A

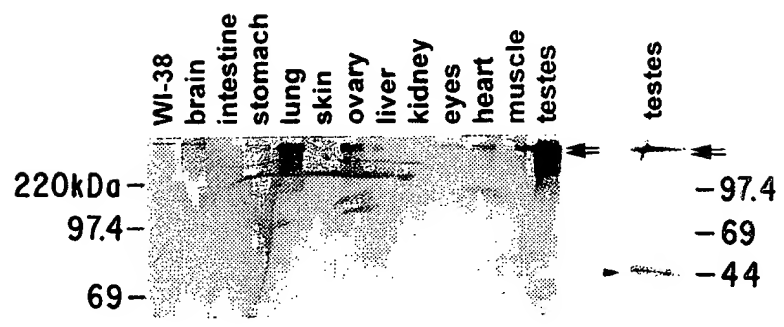


FIG.23B

208070" 2E420660

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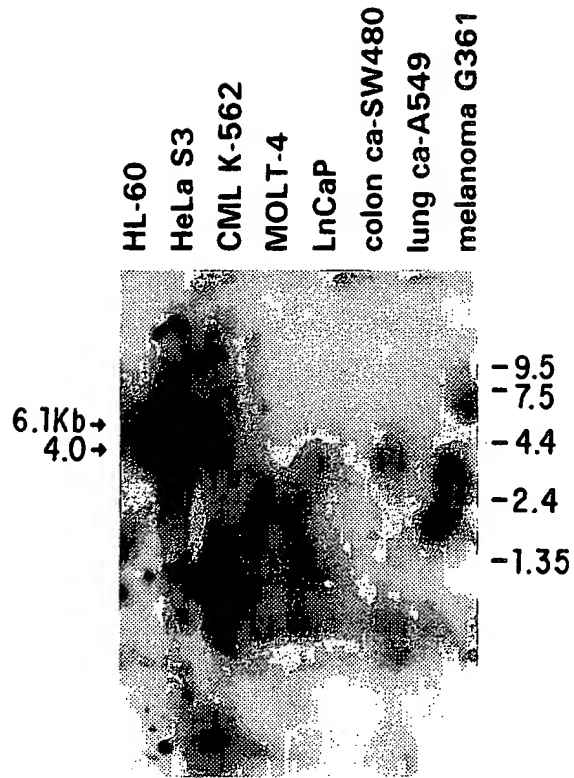


FIG.24

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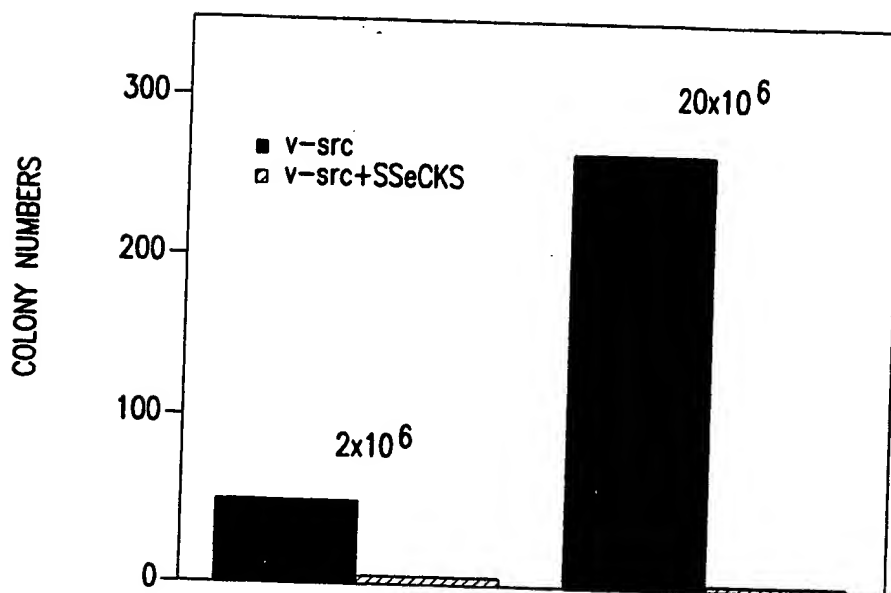


FIG.25A

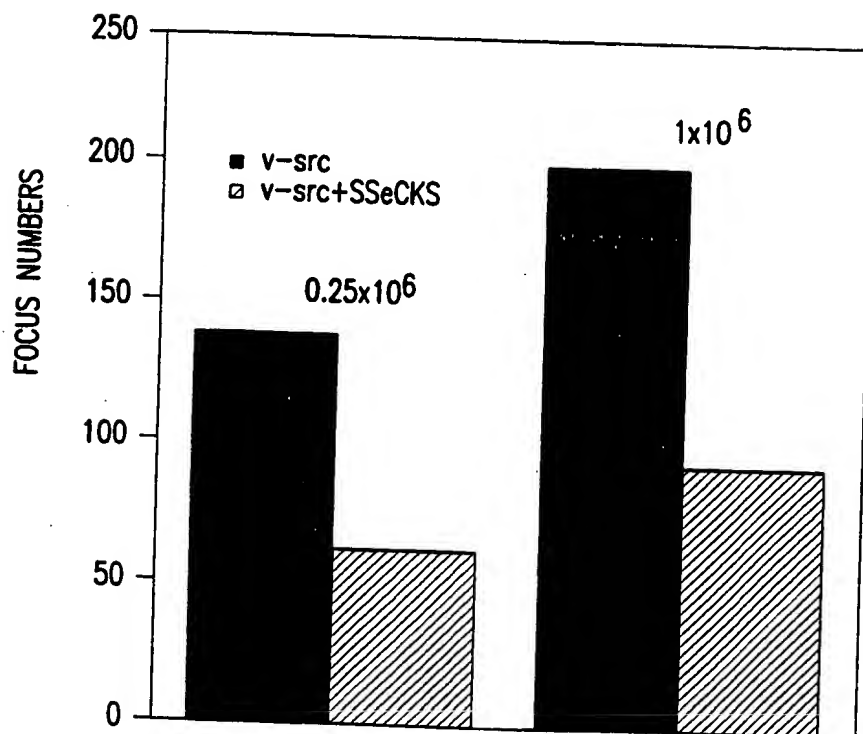


FIG.25B

208040" 2E+20660

(47 of 90)



		<u>Myr.</u>	<u>Pal.</u>
src	MGSSKSKPKD	+	-
yes	MGCIKSKEDK	+	+
SSeCKS	MGAGSSTEQR	+	?
G α t1	MGAGASAEK	+	-
G α i1	MGCTLSAEDK	+	+
GAP-43	MLCCMRRTKQ	-	+

MYRIST. CONSENSUS: MGXXX^S_T

FIG.26

0902432.040802
208040"2E420560

(48 of 90)

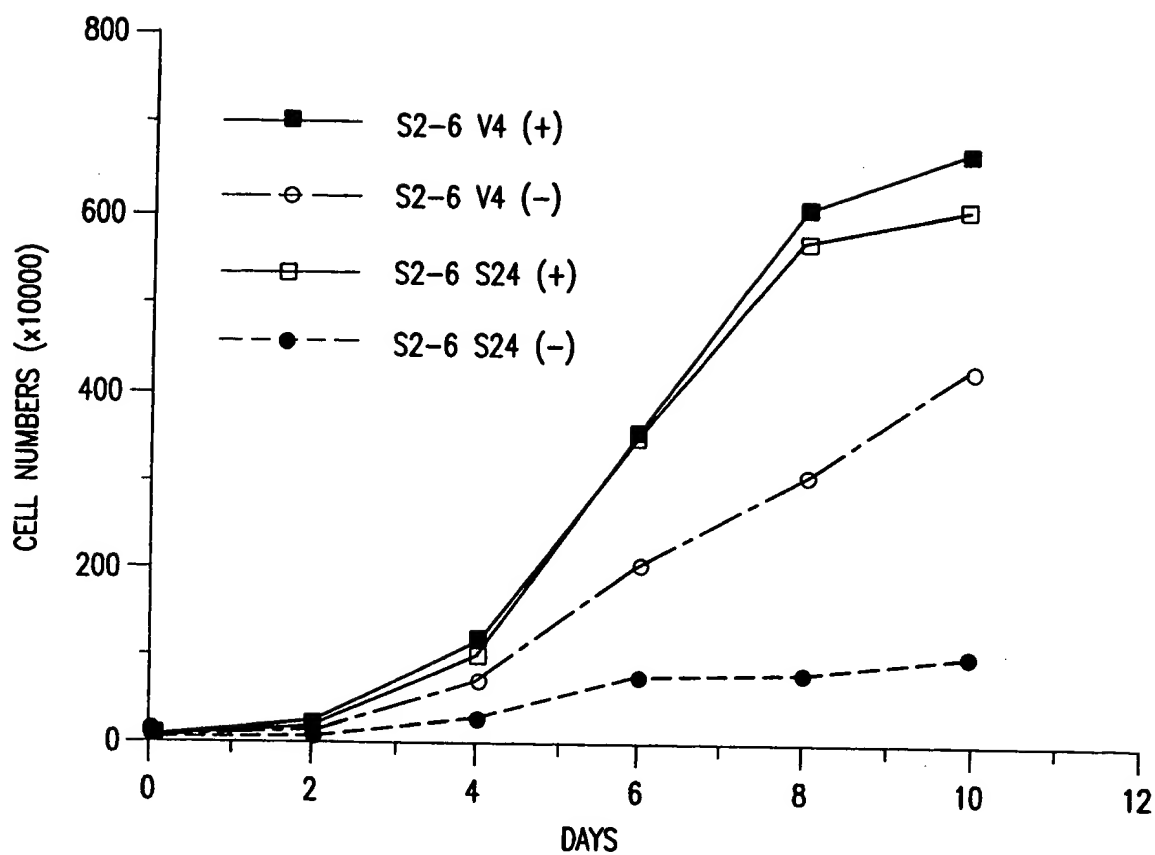


FIG.27

208070" 25-12-60

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Tet + -



- 220kDa

FIG.28

208040"2E420660

208040" 2E420660

(50 of 90)

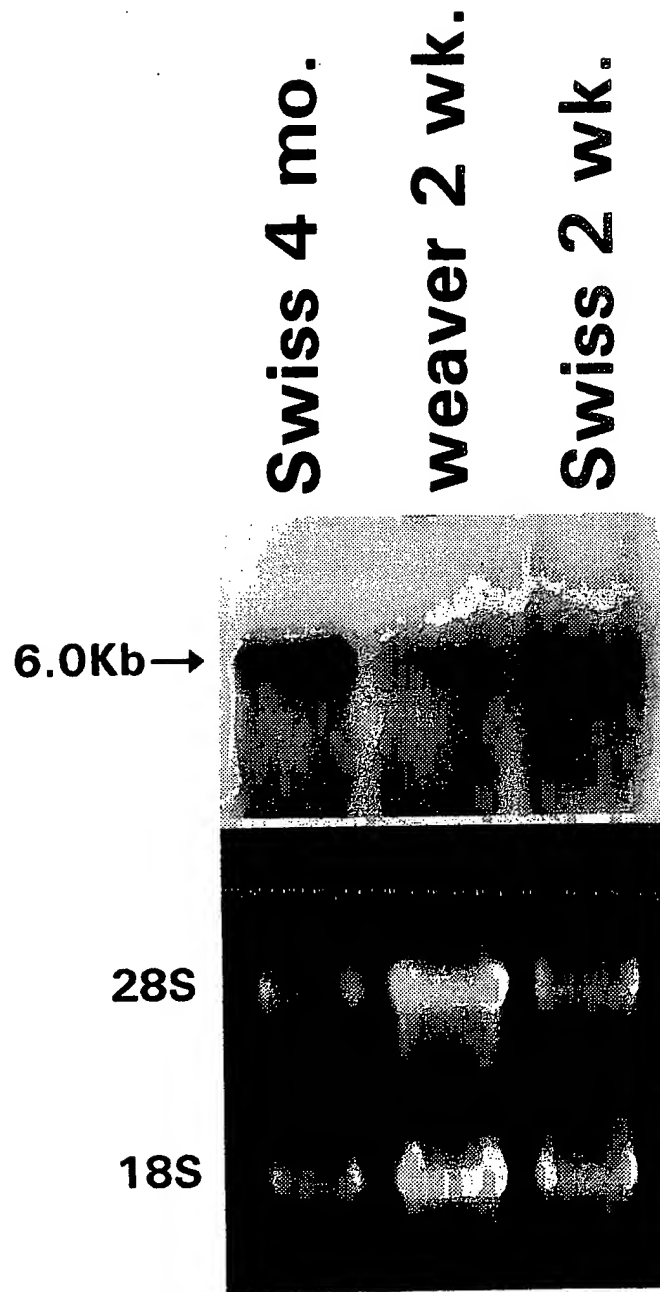


FIG.29



FIG.30A



FIG.30B

208040 2E420660



FIG.30C

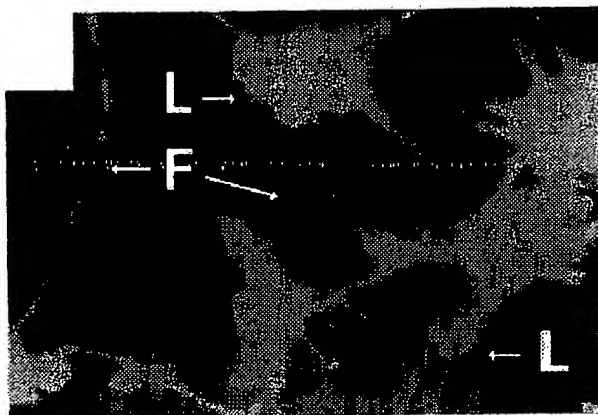


FIG.30D

208040-2E420660

09902432-040802

(53 of 90)



FIG.31A



FIG.31B

0902432 040802

(54 of 90)

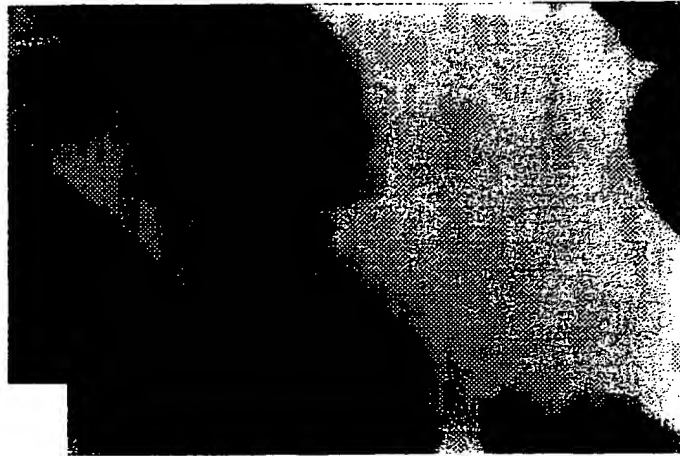


FIG.31C



FIG.31D

208040" 2E420660



FIG.32A

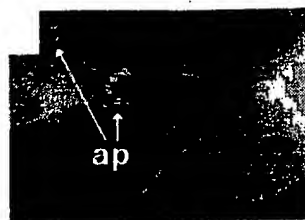


FIG.32B



FIG.32C

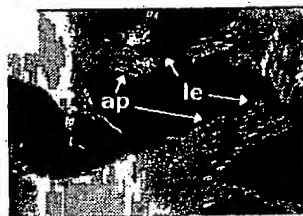


FIG.32D



FIG.32E



FIG.32F



FIG.32G



FIG.32H

(55 of 90)



208040 23420650 0902432 040802



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FIG.33A



FIG.33B



FIG.33C



FIG.33D



FIG.33E

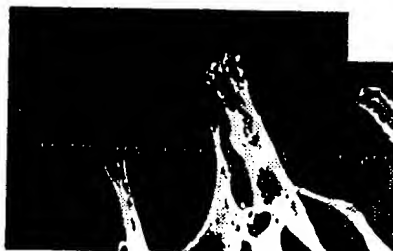


FIG.33F



FIG.33G



FIG.33H

208040" 2E720660

208040"2E720660

(57 of 90)

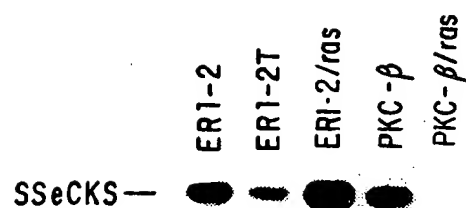


FIG.34



(58 of 90)

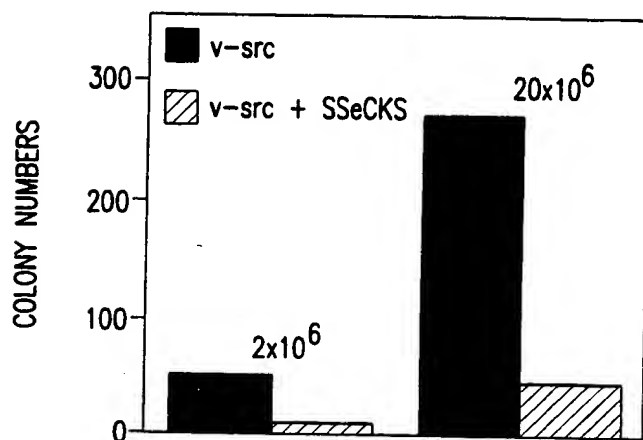


FIG.35A

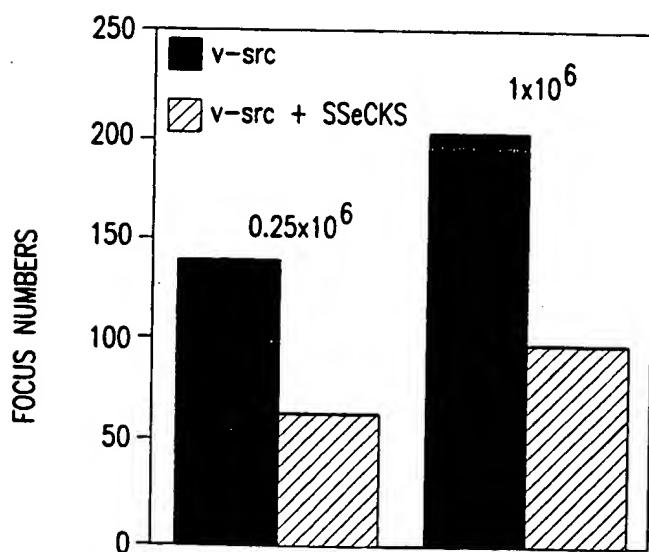
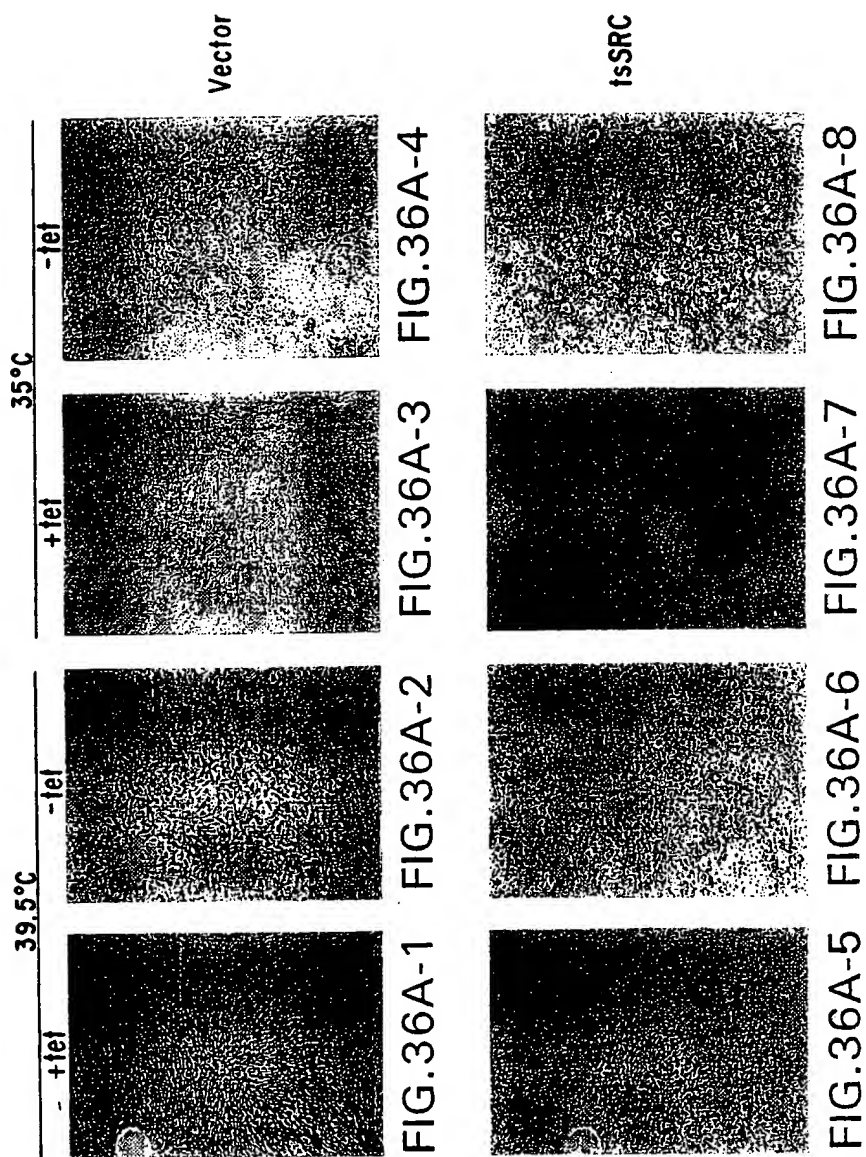


FIG.35B

20250710 23:42:05

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(60 of 90)



35°C

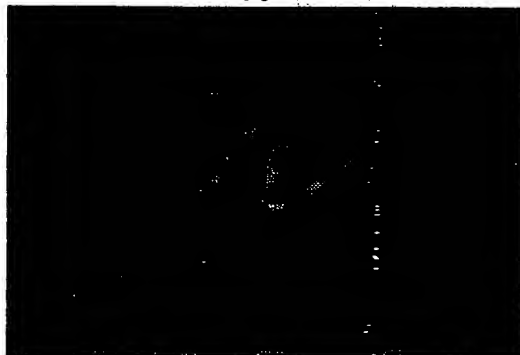


FIG.36B-1

39.5°C



+tet

FIG.36B-2



FIG.36B-3



-tet

FIG.36B-4

208040-28120660



(61 80)

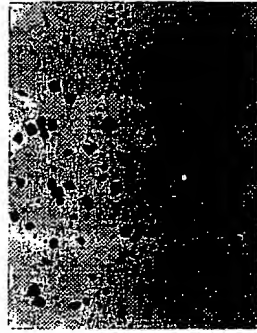


FIG.37A-1



FIG.37A-2

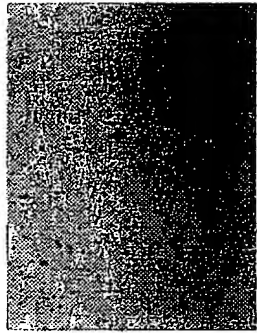


FIG.37A-3

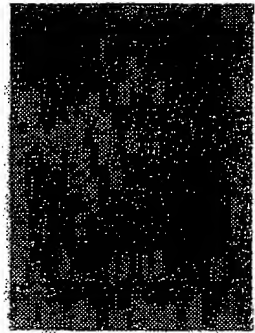
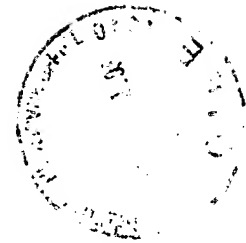


FIG.37A-4

208040" 28420650

(62 of 90)



SOFT AGAR COLONY FORMATION						
	ts src1	ts src2	ts src3	ts src4	pLJ2	pLJ3
+ tet	2160	1640	2800	1080	0	0
- tet	60	60	110	35	0	0

FIG.37B

20230402 23:04:32

(63 of 90)

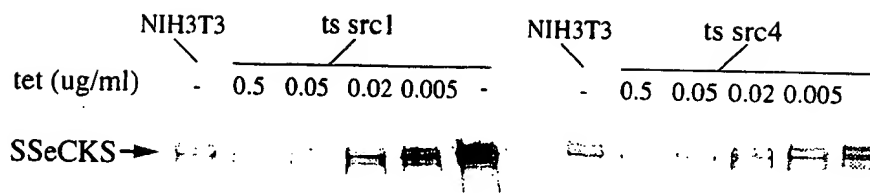


FIG.38A

0.5ug/ml tet

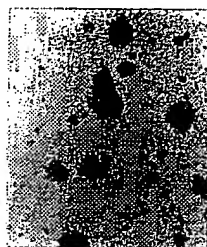


FIG.38C-1

0.02ug/ml tet

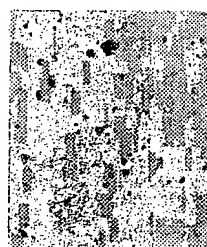
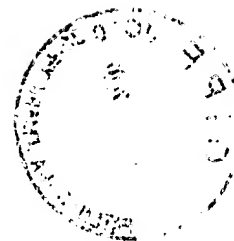


FIG.38C-2

209040" 25420660

203040" 2E420650

(64 of 9



SOFT AGAR COLONY FORMATION					
	35°C				39°C
tet(ug/ml)	0.5	0.05	0.02	0.005	0
ts src1	2852	2464	174	51	22
ts src4	1463	743	67	11	0

FIG.38B



(65 of 90)

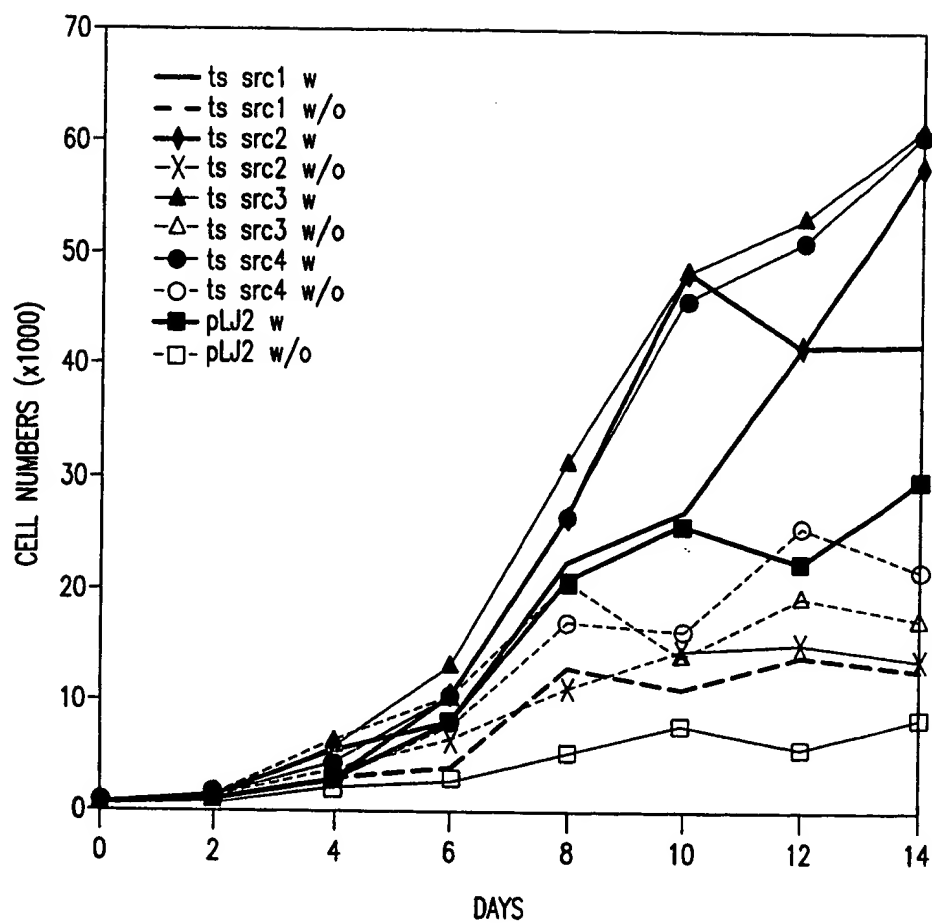


FIG.39A

208040" 2E-720660

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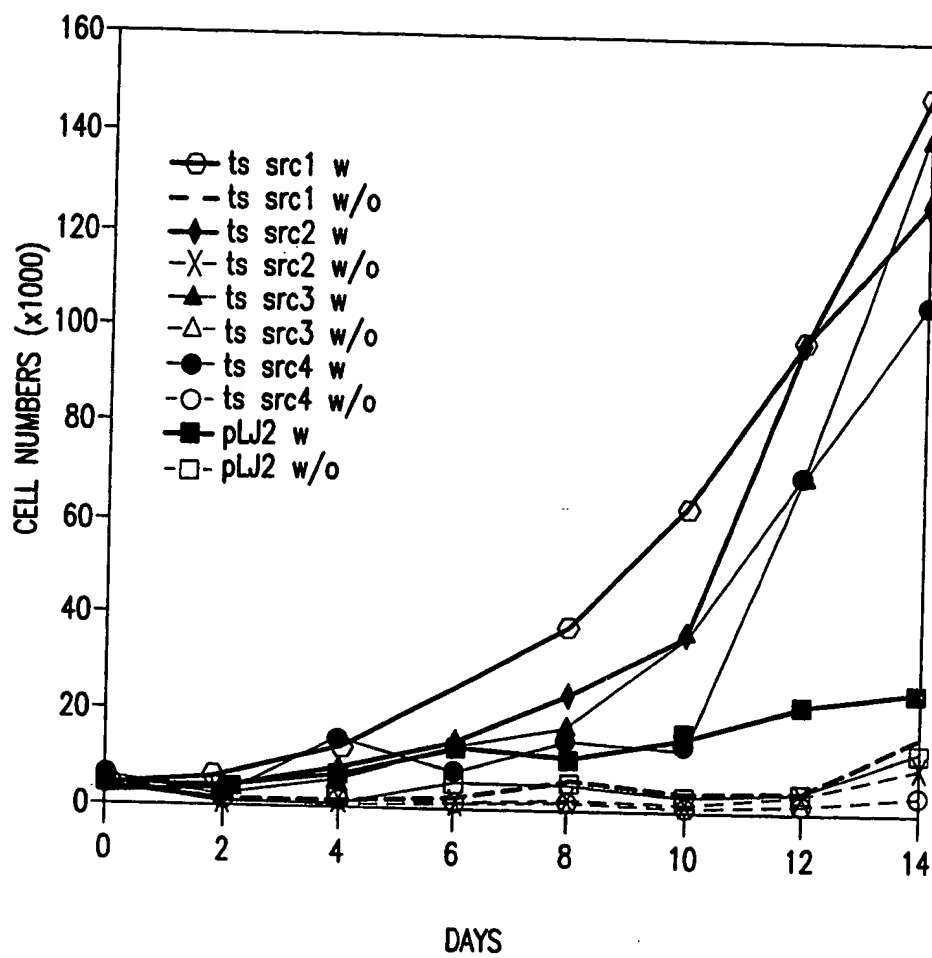


FIG.39B

208040" 22720550

(67 of 90)

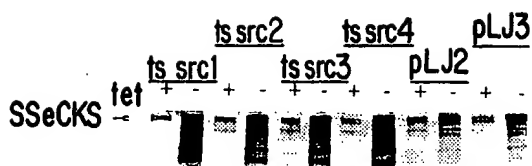


FIG. 40A

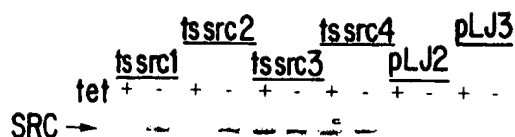


FIG. 40B

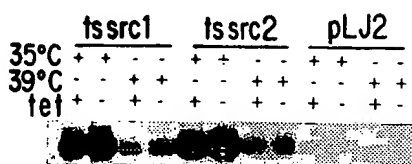


FIG. 40C-1

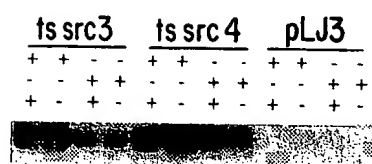


FIG. 40C-2

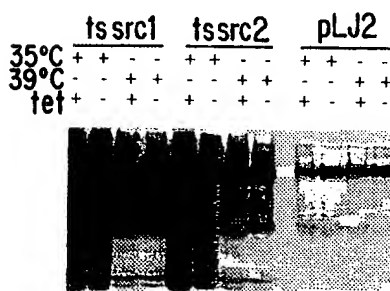


FIG. 40D-1

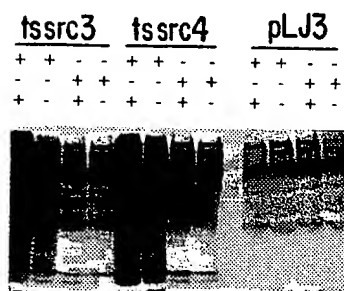


FIG. 40D-2

208040" 2E420650

(68 of 90)

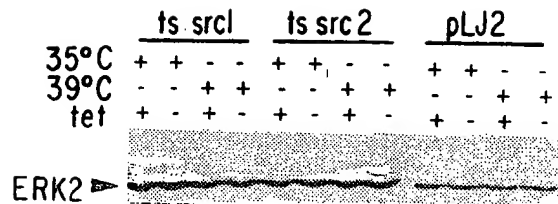


FIG.41A-1

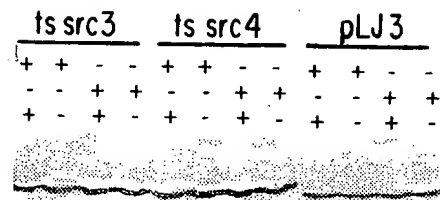


FIG.41A-2

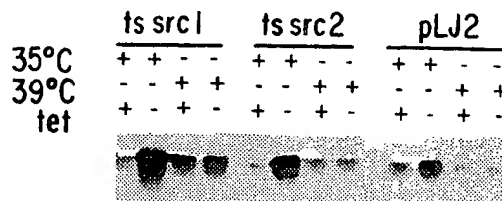


FIG.41B-1

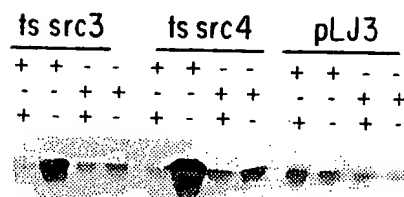


FIG.41B-2

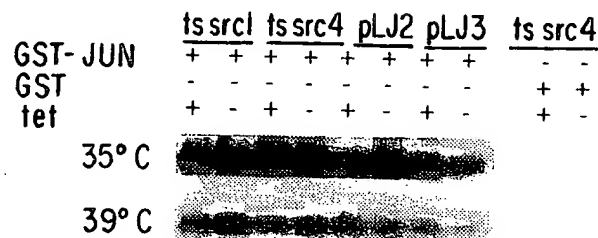


FIG.41C

208040" 2E+20650

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SSeCKS



FIG.42A-1

Vinculin



35°C
+tet

FIG.42A-2



FIG.42A-3



35°C
-tet

FIG.42A-4

208040.232.040802



SSeCKS



FIG.42A-5

Vinculin



39.5°C
+tet

FIG.42A-6



FIG.42A-7



39.5°C
-tet

FIG.42A-8

208040" 2E420650

(710 f 90)



SSeCKS

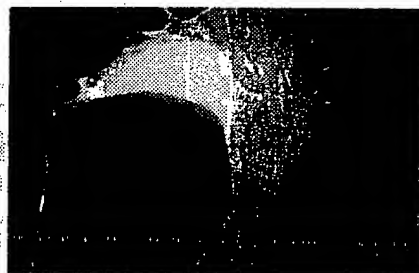
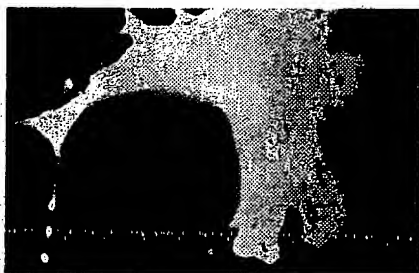
Phalloidin



35°C
+tet

FIG.42B-1

FIG.42B-2



35°C
-tet

FIG.42B-3

FIG.42B-4

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SSeCKS

Phalloidin



FIG.42B-5

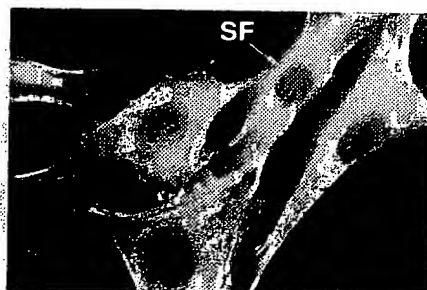


FIG.42B-6

39.5°C
+ tet

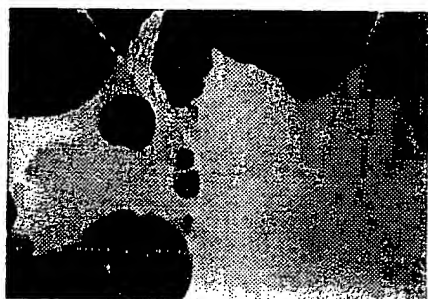


FIG.42B-7



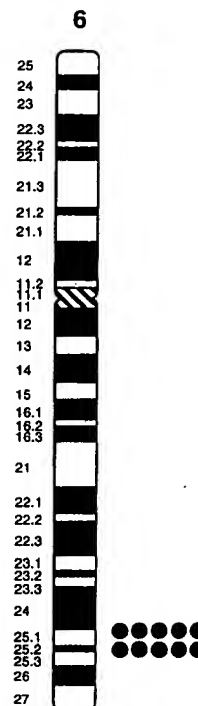
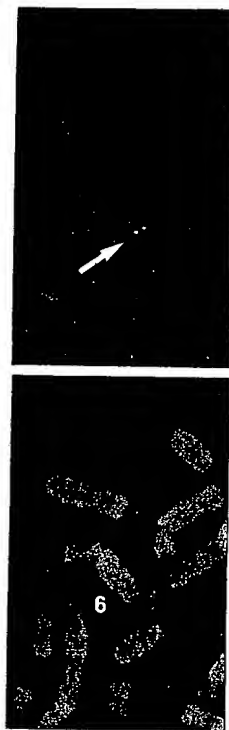
FIG.42B-8

39.5°C
-tet

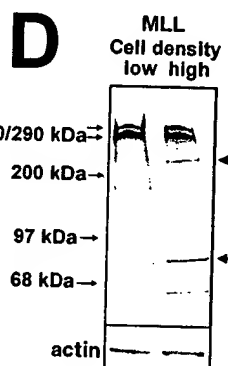
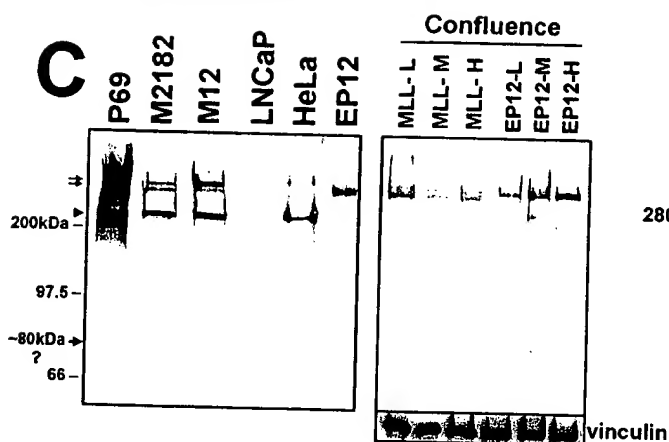
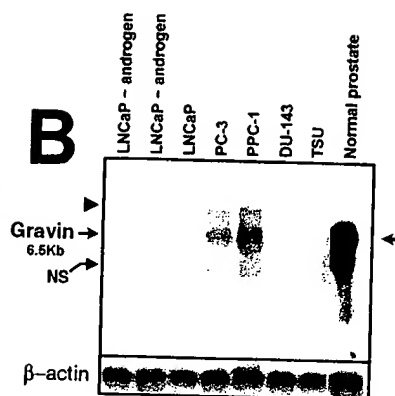
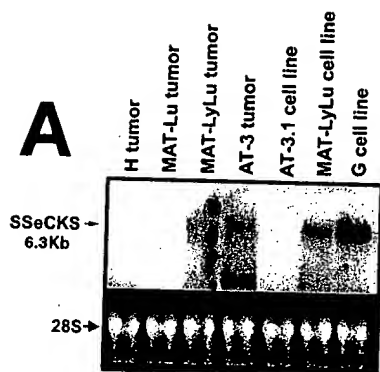
09902432.040302

208040" 23420660

Figure 4
(73 of 90)

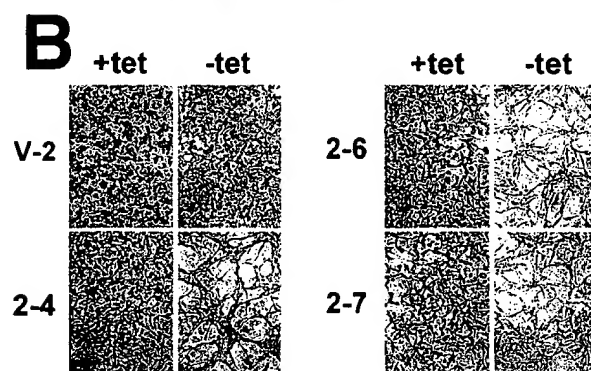
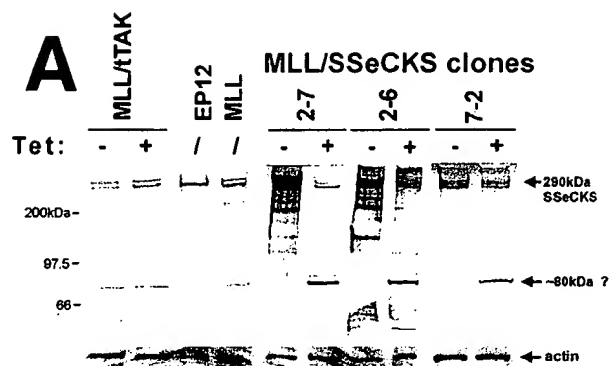


(74 of 90)



208040" 2E1720660

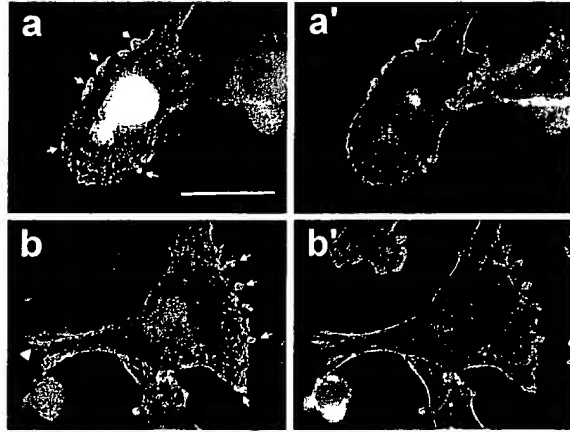
Figure 45
(75 of 90)



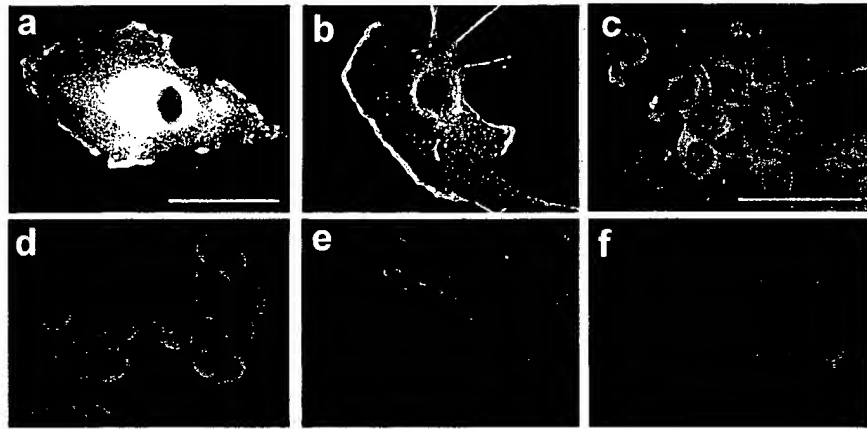
203040-2E420650



A



B



203040" 2E420650

(77 of 90)

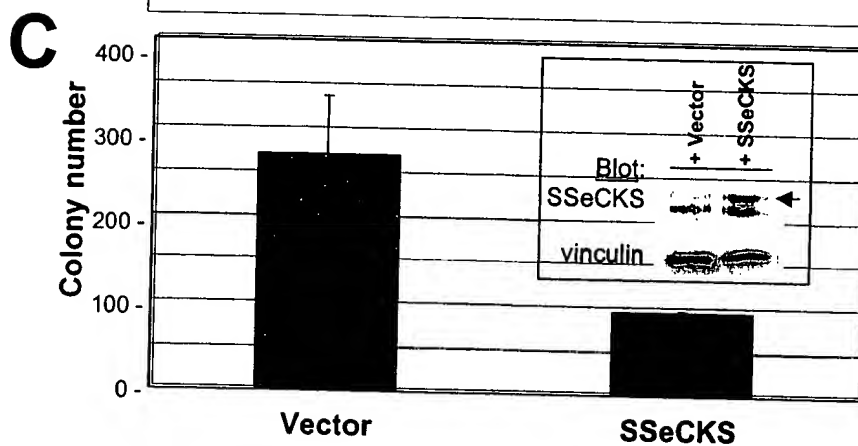
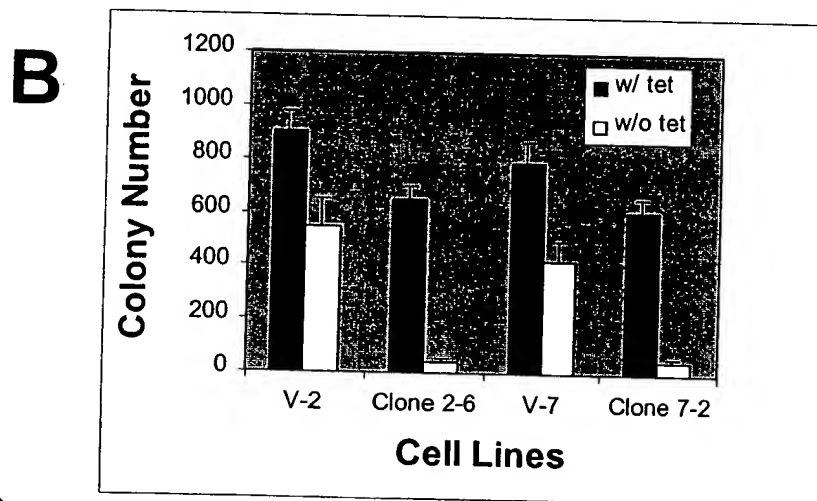
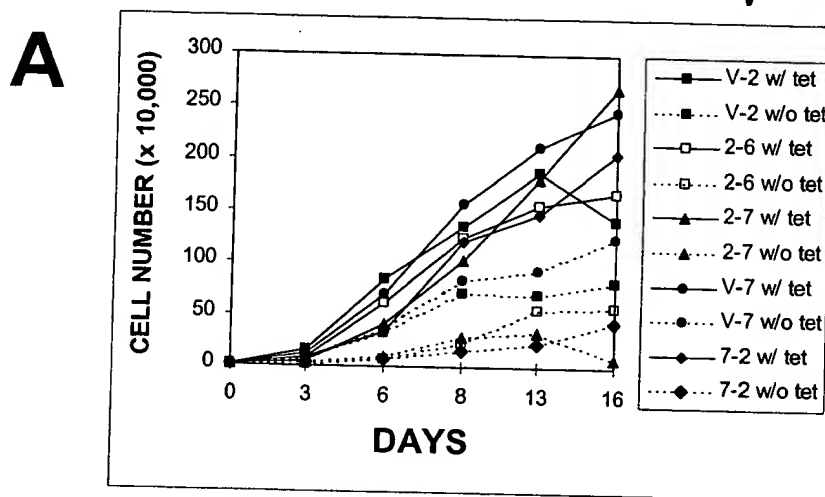


Fig. 47

202040" 2E420650

(78 of 90)

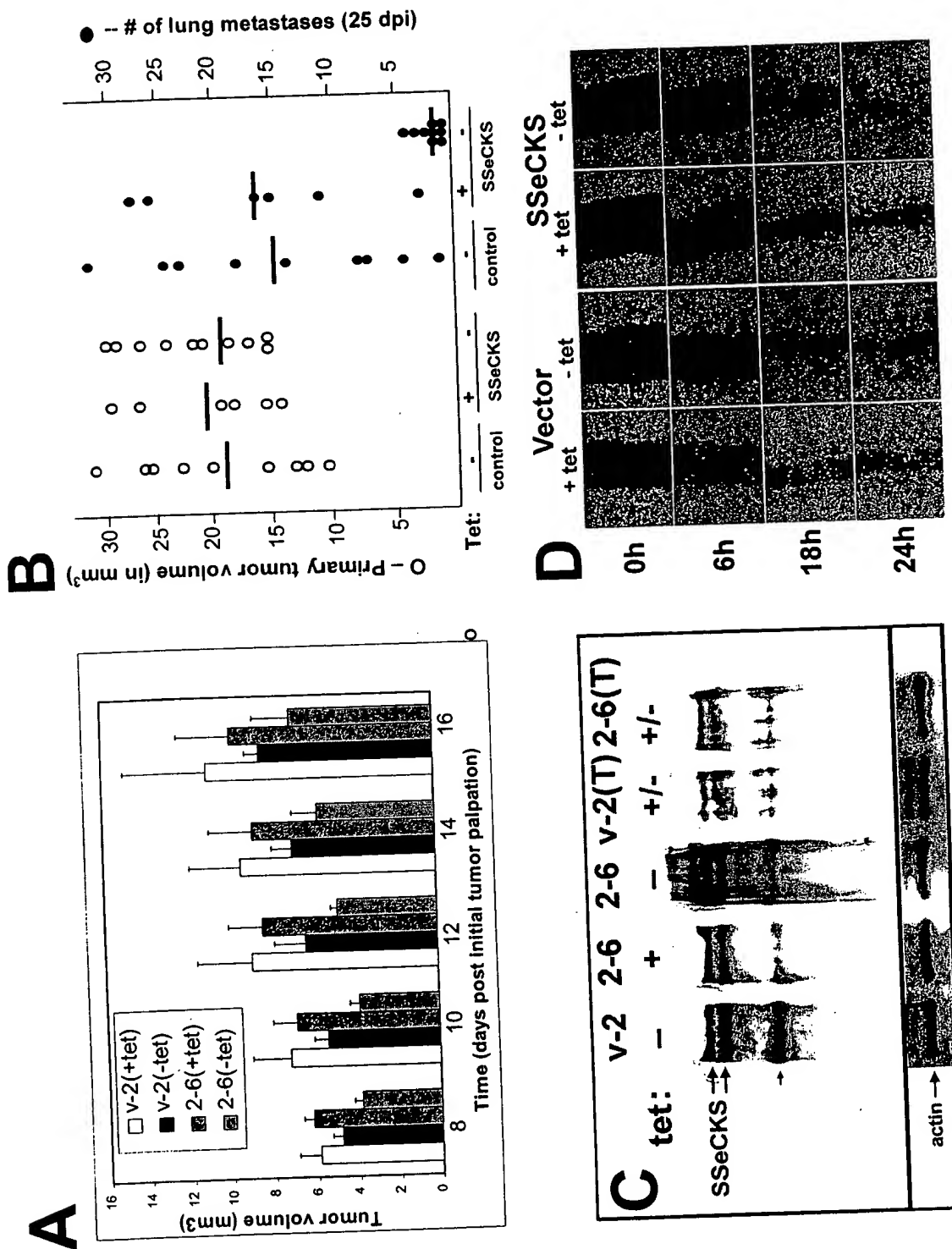


Fig. 48

(79 of 90)

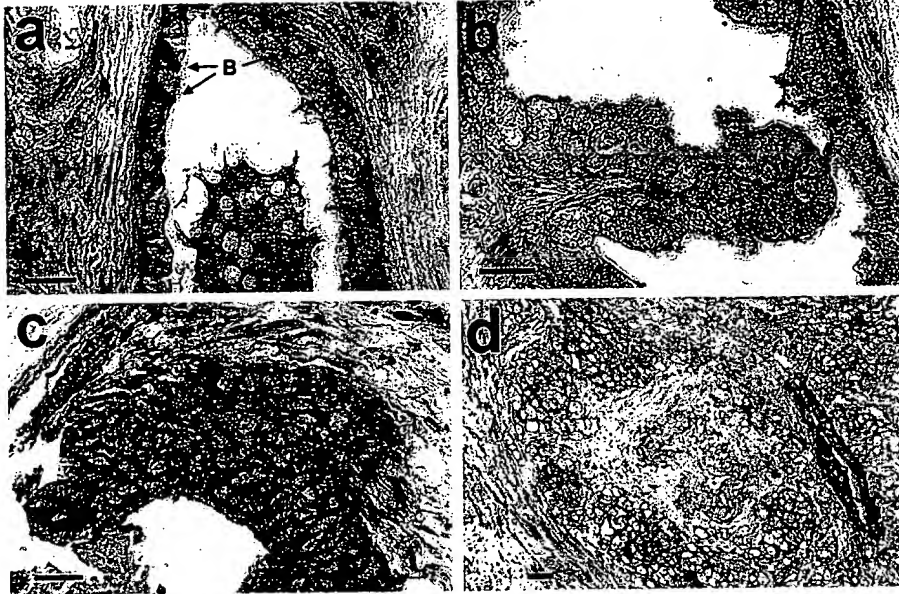


Fig. 49

09902432.040802

(80 of 90)

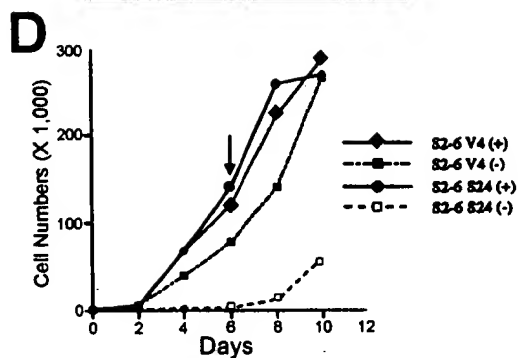
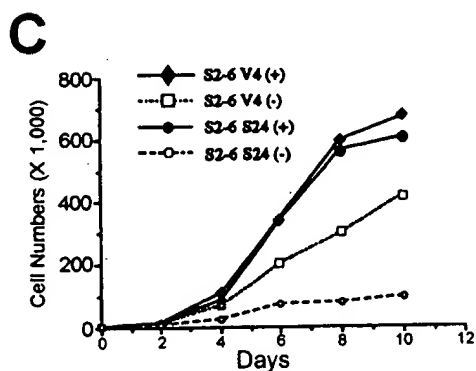
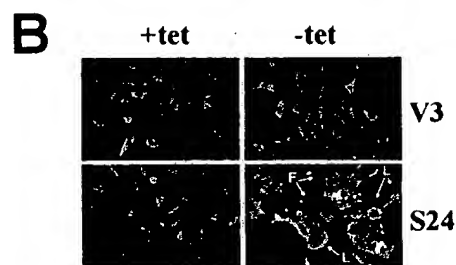
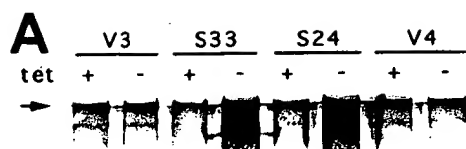


Figure 50

2023040" 23:42:06:50

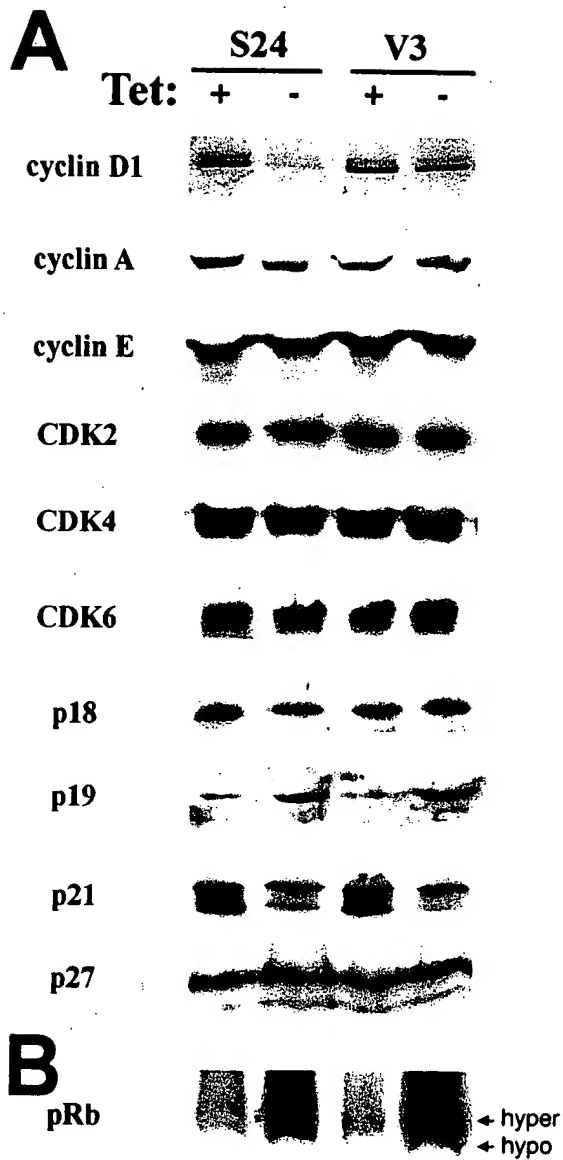


Figure 51

208040"23420660

2009040 2E420560

FA1

(82 of 90)

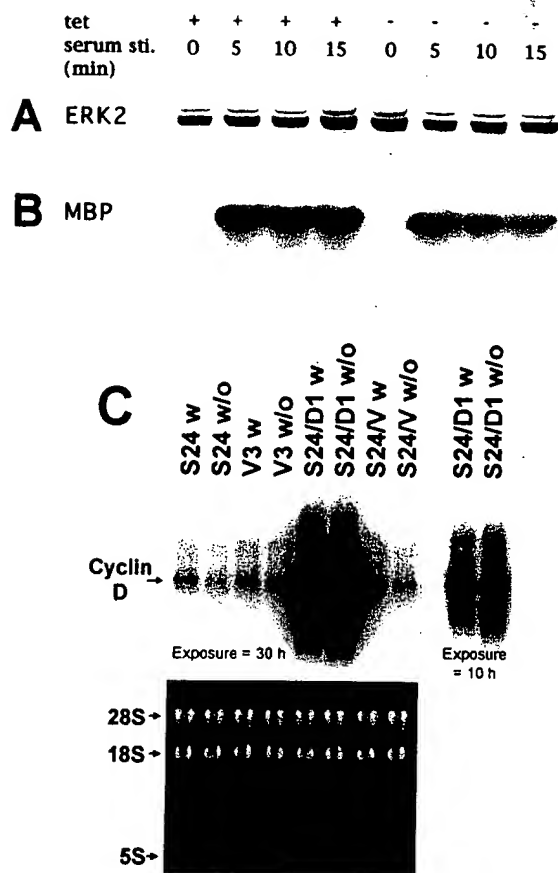


Figure 52

(83 of 90)

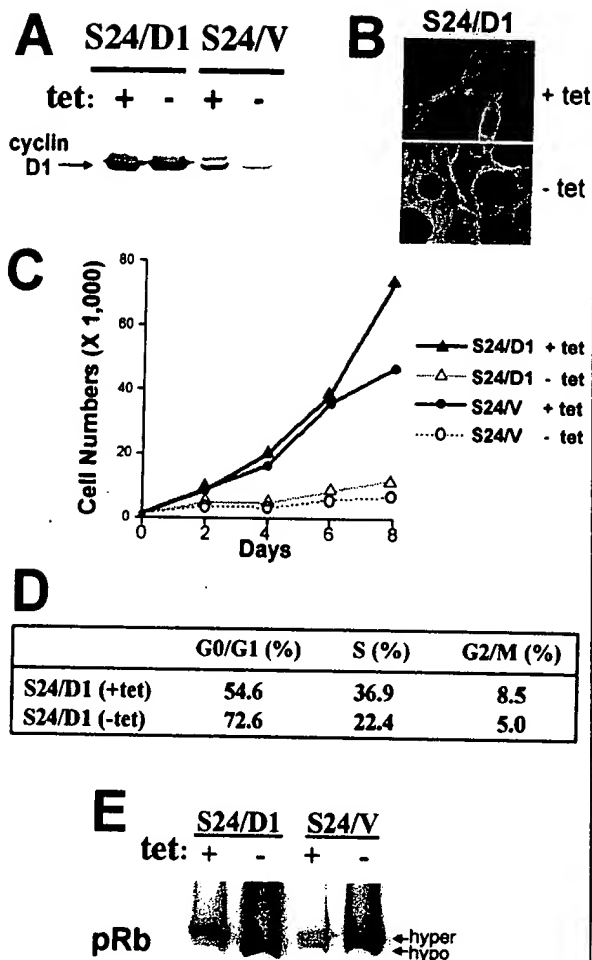


Figure 53

208040"2E720660

SSeCKS

⁴⁶⁸SPEEKTLPKHPEGIVSEVM

LSSQERIK₄₉₆

Newt pRb

|| ||: |||||::| |
⁷⁸⁰SP.LKSPYKHPEGLLSPTKM - (27 a.a.) - LSSSERLR₈₃₄

Figure 54



208040-23720660

(85 of 90)



A

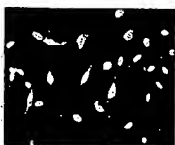
S24/D1
(+tet)



S24/D1
(-tet)



V3/D1
(+tet)



V3/D1
(-tet)



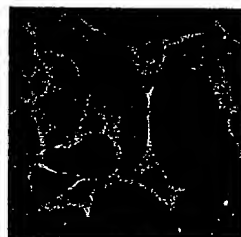
B

SSeCKS

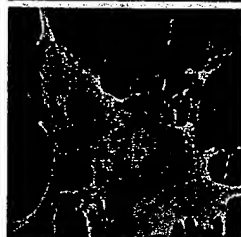
cyclin D1

SSeCKS +
cyclin D1

+ tet



- tet



C

- tet

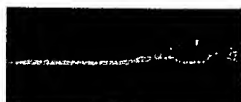


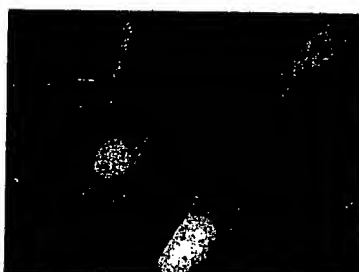
Figure 55

20201027 21:20:50

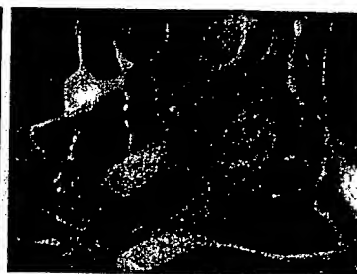
(86 of 90)



S24/D1
+ tet



S24/D1
- tet



S24/D1
+ tet
+ PMA



S24/D1
- tet
+ PMA

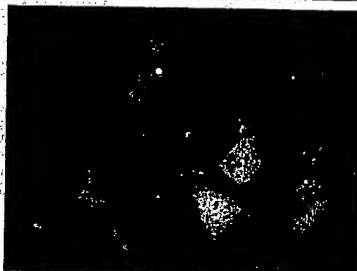


Figure 56

208040 2E720660



(87 of 90)



D1 ↑

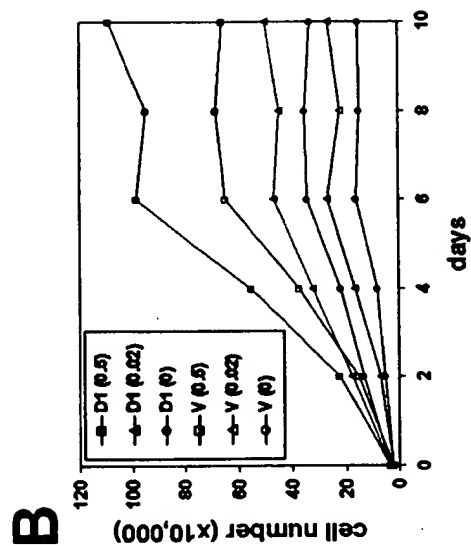
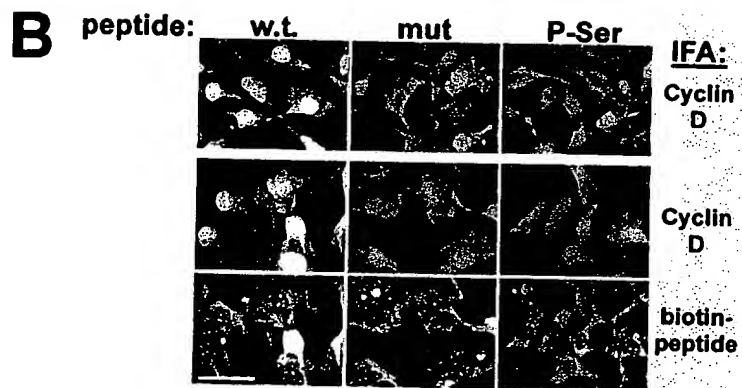
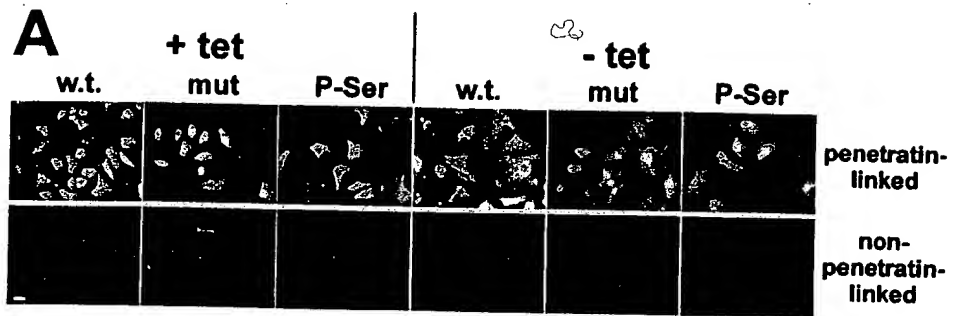
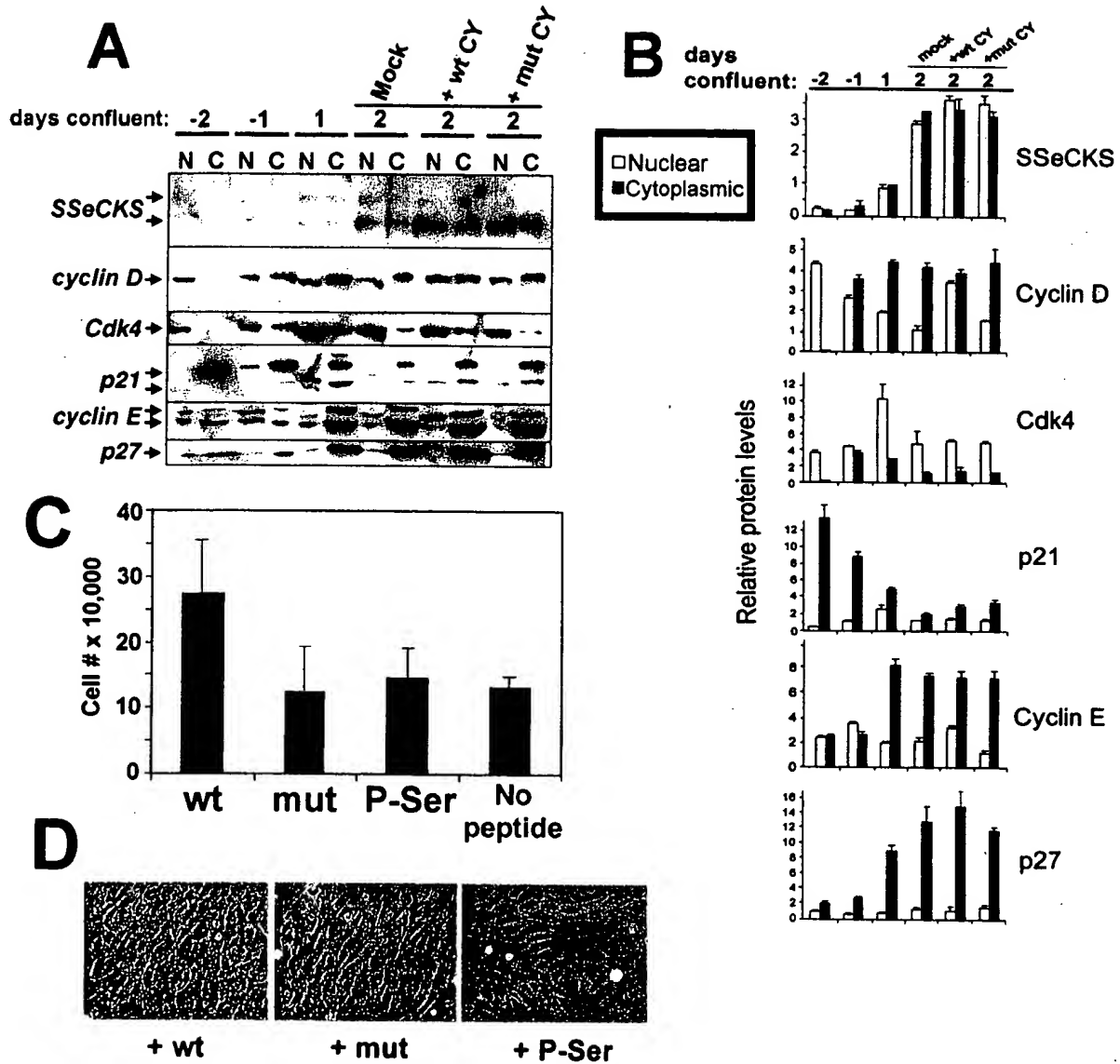


Figure 58
(88 of 90)



208040"2E120660

Figure 59
(89 of 90)



208040 281720660



Figure 60
(90 of 90)

